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* * * * * * * * * *  Welcome to STN International  * * * * * * * * * *

 NEWS  1      Web Page for STN Seminar Schedule - N. America
 NEWS  2  AUG 10  Time limit for inactive STN sessions doubles to 40
          minutes
 NEWS  3  AUG 18  COMPENDEX indexing changed for the Corporate Source
          (CS) field
 NEWS  4  AUG 24  ENCOMPLIT/ENCOMPLIT2 reloaded and enhanced
 NEWS  5  AUG 24  CA/CAplus enhanced with legal status information for
          U.S. patents
 NEWS  6  SEP 09  50 Millionth Unique Chemical Substance Recorded in
          CAS REGISTRY
 NEWS  7  SEP 11  WPIDS, WPINDEX, and WPIX now include Japanese FTERM
          thesaurus
 NEWS  8  OCT 21  Derwent World Patents Index Coverage of Indian and
          Taiwanese Content Expanded
 NEWS  9  OCT 21  Derwent World Patents Index enhanced with human
          translated claims for Chinese Applications and Utility Models
 NEWS 10  NOV 23  Addition of SCAN format to selected STN databases
 NEWS 11  NOV 23  Annual Reload of IFI Databases
 NEWS 12  DEC 01  FRFULL Content and Search Enhancements
 NEWS 13  DEC 01  DGENE, USGENE, and PCTGEN: new percent identity
          feature for sorting BLAST answer sets
 NEWS 14  DEC 02  Derwent World Patent Index: Japanese FI-TERM
          thesaurus added
 NEWS 15  DEC 02  PCTGEN enhanced with patent family and legal status
          display data from INPADOCDB
 NEWS 16  DEC 02  USGENE: Enhanced coverage of bibliographic and
          sequence information
 NEWS 17  DEC 21  New Indicator Identifies Multiple Basic Patent
          Records Containing Equivalent Chemical Indexing in CA/CAplus
 NEWS 18  JAN 12  Match STN Content and Features to Your Information
          Needs, Quickly and Conveniently
 NEWS 19  JAN 25  Annual Reload of MEDLINE database

 NEWS EXPRESS MAY 26 09 CURRENT WINDOWS VERSION IS V8.4,
          AND CURRENT DISCOVER FILE IS DATED 06 APRIL 2009.

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FILE LAST UPDATED: 5 Feb 2010  (20100205/ED)
REVISED CLASS FIELDS (/NCL) LAST RELOADED:  Dec 2009
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE:  Oct 2009

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=> s ((express?(w)profil?) or (express?(w)pattern?) or proteom? or (express?(w)measur?))/bi,ab   1674701 EXPRESS?/BI
 1568072 EXPRESS?/AB
  590515 PROFIL?/BI
  521816 PROFIL?/AB
   68323 EXPRESS?(W)PROFIL?
 1674701 EXPRESS?/BI
 1568072 EXPRESS?/AB
  924755 PATTERN?/BI
  875830 PATTERN?/AB
   40623 EXPRESS?(W)PATTERN?
   38960 PROTEOM?/BI
   29773 PROTEOM?/AB
 1674701 EXPRESS?/BI
 1568072 EXPRESS?/AB
 3490453 MEASUR?/BI
 3324616 MEASUR?/AB
    1127 EXPRESS?(W)MEASUR?
L1      132667 (((EXPRESS?(W)PROFIL?) OR (EXPRESS?(W)PATTERN?) OR PROTEOM? OR (EXPRESS?(W)MEASUR?))/BI,AB

=> s (drug? or activ?)/bi,ab   1110477 DRUG?/BI
  678226 DRUG?/AB
 4720298 ACTIV?/BI
 4214268 ACTIV?/AB
L2      5475133 (DRUG? OR ACTIV?)/BI,AB

=> s l1 and l2
L3      47366 L1 AND L2
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=> s (chang? or shift? or differ?)/bi,ab   2619616 CHANG?/BI
2468506 CHANG?/AB
SYSTEM LIMITS EXCEEDED - SEARCH ENDED
The search profile you entered was too complex or gave too
many
answers.  Simplify or subdivide the query and try again.  If you
have
exceeded the answer limit, enter DELETE HISTORY at an arrow
prompt
(=>) to remove all previous answers sets and begin at L1.  Use
the
SAVE command to store any important profiles or answer sets
before
using DELETE HISTORY.

=> s (chang? or shift? or differ?)/bi,ab   2619616 CHANG?/BI
2468506 CHANG?/AB
SYSTEM LIMITS EXCEEDED - SEARCH ENDED
The search profile you entered was too complex or gave too
many
answers.  Simplify or subdivide the query and try again.  If you
have
exceeded the answer limit, enter DELETE HISTORY at an arrow
prompt
(=>) to remove all previous answers sets and begin at L1.  Use
the
SAVE command to store any important profiles or answer sets
before
using DELETE HISTORY.

=> s l2 and (chang? or shift? or differ?)/bi,ab   2619616
CHANG?/BI              2468506 CHANG?/AB              564778
SHIFT?/BI               544027 SHIFT?/AB             4859272
DIFFER?/BI             4637317 DIFFER?/AB
L4      1652650 L2 AND (CHANG? OR SHIFT? OR DIFFER?)/BI,AB
 75% OF LIMIT FOR TOTAL ANSWERS REACHED

=> s (((express?(w)profil?) or (express?(w)pattern?) or proteom?
or (express?(w)measur?))(10a)(chang? or shift? or
differ?)(10a)(drug? or activ? or therapeut?))/bi,ab   1674701
EXPRESS?/BI            1568072 EXPRESS?/AB
590515 PROFIL?/BI               521816 PROFIL?/AB
1674701 EXPRESS?/BI            1568072 EXPRESS?/AB
924755 PATTERN?/BI              875830 PATTERN?/AB
38960 PROTEOM?/BI                29773 PROTEOM?/AB
1674701 EXPRESS?/BI            1568072 EXPRESS?/AB
3490453 MEASUR?/BI              3324616 MEASUR?/AB
2619616 CHANG?/BI              2468506 CHANG?/AB
564778 SHIFT?/BI                544027 SHIFT?/AB
4859272 DIFFER?/BI             4637317 DIFFER?/AB
1110477 DRUG?/BI                678226 DRUG?/AB
4720298 ACTIV?/BI              4214268 ACTIV?/AB
346412 THERAPEUT?/BI            286595 THERAPEUT?/AB
L5      1153 (((EXPRESS?(W)PROFIL?) OR
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(EXPRESS?(W)MEASUR?))(10A)(CHANG? OR SHIFT? OR
DIFFER?)(10A)(DRU       G? OR ACTIV? OR
THERAPEUT?))/BI,AB

=> s l5 not 2010/py   162342 2010/PY
L6      1134 L5 NOT 2010/PY

=> s l6 not 2009/py   1774345 2009/PY
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=> s l7 not 2008/py   1787991 2008/PY
L8      820 L7 NOT 2008/PY

=> s l8 not 2007/py   1718936 2007/PY
L9      674 L8 NOT 2007/PY

=> s l9 not 2006/py   1586614 2006/PY
L10     528 L9 NOT 2006/PY

=> s l10 not 2005/py   1433148 2005/PY
L11     420 L10 NOT 2005/PY

=> s l11 not 2004/py   1352160 2004/PY
L12     296 L11 NOT 2004/PY

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 (FILE 'HOME' ENTERED AT 12:40:20 ON 06 FEB 2010)
 FILE 'CAPLUS' ENTERED AT 12:40:32 ON 06 FEB 2010
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L2      5475133 S (DRUG? OR ACTIV?)/BI,AB
L3      47366 S L1 AND L2
L4      1652650 S L2 AND (CHANG? OR SHIFT? OR
DIFFER?)/BI,AB
L5      1153 S (((EXPRESS?(W)PROFIL?) OR
(EXPRESS?(W)PATTERN?) OR PROTEOM? O
L6      1134 S L5 NOT 2010/PY
L7      960 S L6 NOT 2009/PY
L8      820 S L7 NOT 2008/PY
L9      674 S L8 NOT 2007/PY
L10     528 S L9 NOT 2006/PY
L11     420 S L10 NOT 2005/PY
L12     296 S L11 NOT 2004/PY

=> d l12 1-296 bib ab

L12 ANSWER 1 OF 296  CAPLUS  COPYRIGHT 2010 ACS on STN
AN  2005:514457  CAPLUS <<LOGINID::20100206>>
DN  143:453665
TI  Expression of human growth hormone in potato plants
AU  Esmat, Jourabchi; Sohi. Halleh, Hashemi; Hatef, Salmanian
Ali; Amir, Mosavi
CS  National Research Center for Genetic Engineering and
Biotechnology, Tehran, 14155-6343, Iran
SO  Majmoa-i Maghalat-i Sevomin Hemayesh Maliy
Biotechnology Jomhoriy-i Islame-i Iran, Mashhad, Islamic
Republic of Iran, Sept. 9-11, 2003 (2003), Volume 2, 15-18
Publisher: Danishgah-i Ferdowsi Mashhad, Mashhad, Iran.
CODEN: 69GXPF; ISBN: 964-386-023-X
DT  Conference
LA  Persian
AB  In addn. to their traditional role as a source of natural
medicines it is now possible to genetically engineer plants to
produce biopharmaceuticals. Transgenic plants expressing
biopeptides offer many advantage as a low-cost prodn. systems
and effective delivery vehicle.  Among bioactive peptides human
growth hormone (hGh) is the one of the most attractive, esp. if it
can be used directly in the treatment of hypopituitary dwarfism in
children or other related syndromes.  In this study, at first the
cDNA of hGH was cloned in different plant expression vectors
under the control of CaMV35S, pPatatin promoters.  These
constructs transformed to potato plants.  Regeneration plants
grew later and are transferred to the soil and greenhouse.  The
current focus of attention would be on anal. of hGH
***expression***  ***pattern***  in  ***different***
tissue of transgenic plants and to det. its biol.  ***activity***  .
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L12 ANSWER 2 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2005:404056 CAPLUS <<LOGINID::20100206>>
DN 143:112634
TI The proteome of neural stem cells from adult rat hippocampus
AU Maurer, Martin H.; Feldmann, Robert E., Jr.; Fuetterer, Carsten D.; Kuschinsky, Wolfgang
CS Dept. of Physiology and Pathophysiology, University of Heidelberg, Heidelberg, 69120, Germany
SO Proteome Science (2003), 1, No pp. given CODEN: PSRCCC; ISSN: 1477-5956 URL: http://www.proteomesci.com/content/pdf/1477-5956-1-4.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Hippocampal neural stem cells (HNSC) play an important role in cerebral plasticity in the adult brain and may contribute to tissue repair in neurol. disease. To describe their biol. potential with regard to plasticity, proliferation, or differentiation, it is important to know the cellular compn. of their proteins, subsumed by the term proteome. Here, we present for the first time a proteomic database for HNSC isolated from the brains of adult rats and cultured for 10 wk. Cytosolic proteins were extd. and subjected to two-dimensional gel electrophoresis followed by protein identification through mass spectrometry, database search, and gel matching. We could map about 1141.+-.209 (N = 5) protein spots for each gel, of which 266 could be identified. We could group the identified proteins into several functional categories including metab., protein folding, energy metab. and cellular respiration, as well as cytoskeleton, Ca2+ signaling pathways, cell cycle regulation, proteasome and protein degrdn. We also found proteins belonging to detoxification, neurotransmitter metab., intracellular signaling pathways, and regulation of DNA transcription and RNA processing. Conclusions: The HNSC ***proteome*** database is a useful inventory which will allow to specify ***changes*** in the cellular protein ***expression*** ***pattern*** due to specific ***activated*** or suppressed pathways during ***differentiation*** or proliferation of neural stem cells. Several proteins could be identified in the HNSC ***proteome*** which are related to ***differentiation*** and plasticity, indicating ***activated*** functional pathways. Moreover, we found a protein for which no expression has been described in brain cells before.
RE CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 3 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2004:483508 CAPLUS <<LOGINID::20100206>>
DN 141:407928
TI Enzyme-targeting small-molecule probes for proteomics applications
AU Huang, Xuan; Tan, Eunice L. P.; Chen, Grace Y. J.; Yao, Shao Q.
CS Department of Chemistry, National University of Singapore, Singapore
SO Applied Genomics and Proteomics (2003), 2(4), 225-238 CODEN: AGPPCU; ISSN: 1175-5644
PB Open Mind Journals Ltd
DT Journal; General Review
LA English
AB A review. In the current post-genomic era, the focus of biol. research is shifting from genome to proteome. Enzymes, which catalyze various biochem. reactions in cells, make up an important part of the proteome in any given organism. Although techniques such as two-dimensional gel electrophoresis (2D-GE) followed by mass spectrometry (MS), liq. chromatog. (LC)-MS/MS, and isotope-coded affinity tag (ICAT) make it possible to quant. profile the entire ***proteome*** of an organism, ***activity*** -based profiling of ***different*** subsets of proteins (eg ***different*** classes of enzymes) in a complex ***proteome*** , or the subproteome, remains a formidable challenge. This has led to a resurgent pursuit in the development of enzyme-targeting small-mol. probes, which are capable of profiling, in vitro as well as in vivo, specific classes of enzymes based only on their inherent catalytic activities. Here, we review recent developments of these probes and their applications in the field of proteomics.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 4 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2004:483506 CAPLUS <<LOGINID::20100206>>
DN 141:203831
TI Transcriptional profiling of angiogenically activated endothelial cells: gene expression reflects the angiogenic stage
AU van Beijnum, Judy R.; Griffioen, Arjan W.
CS Angiogenesis Laboratory, Departments of Internal Medicine and Pathology, Maastricht University Hospital, Maastricht, Neth.
SO Applied Genomics and Proteomics (2003), 2(4), 207-223 CODEN: AGPPCU; ISSN: 1175-5644
PB Open Mind Journals Ltd.
DT Journal; General Review
LA English
AB A review. In vitro models have been used extensively to map gene expression in endothelial cells, but few studies have used cells directly from in vivo sources. Here, the authors compare different gene expression surveys on both culture- and fresh tissue-derived endothelial cells; it emerges that gene expression profiles can be paralleled with the angiogenic stage of the cells. Endothelial cells stimulated with ***different*** growth factors in monolayer culture exhibit gene ***expression*** ***profiles*** indicative of an ***active*** proliferative state, whereas tube formation in vitro induces genes implicated in cell adhesion processes. Genes expressed in tumor endothelial cells are biased towards extracellular matrix remodeling, a late event in angiogenesis. The elucidation of gene expression profiles under these different conditions will lead to a better understanding of the mol. mechanisms during angiogenesis in both pathol. and physiol. circumstances and will have implications for the development of angiogenesis-interfering treatment strategies.
RE CNT 157 THERE ARE 157 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 5 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2004:124158 CAPLUS <<LOGINID::20100206>>
DN 140:143725
TI Differential gene-expression profiling in the leukemia cell lines derived from indolent and aggressive phases of CD56+ T-cell large granular lymphocyte leukemia
AU Daibata, Masanori; Matsuo, Yoshinobu; Machida, Hisanori; Taguchi, Takahiro; Ohtsuki, Yuji; Taguchi, Hirokuni
CS Department of Hematology and Respiratory Medicine, Kochi Medical School, Kochi, Japan
SO International Journal of Cancer (2003), Volume Date 2004, 108(6), 845-851 CODEN: IJCNAW; ISSN: 0020-7136

PB Wiley-Liss, Inc.
DT Journal
LA English
AB As a rule, T cell large granular lymphocyte (T-LGL) leukemia runs a chronic clin. course without need for therapy. Some cases, however, progress to an aggressive disease after the indolent clin. stage. The transformation mechanism into a high-grade malignancy has not been well studied. We have established 2 leukemia cell lines, MOTN-1 and PLT-2, derived from the same clone of CD56+ T-LGL leukemia in chronic and aggressive phases, resp. The paired availability of such cell lines is valuable in biol. and genetic investigation of T-LGL leukemia. We used a microarray contg. 406 cDNAs to elucidate alterations of gene expression between the 2 cell lines. We found a no. of genes that were differentially expressed: 13 genes with increased expression and 3 genes with reduced expression in PLT-2 cells as compared to MOTN-1 cells. Increased expression of the dek, rac, Op18, CD6, CD58, CD106, Id2, ATF4, IRF5, ELL2 and D6 genes, and reduced expression of the GzmA and GzmK genes were confirmed by real-time quant. reverse transcription-PCR, whose results paralleled the microarray data. These upregulated genes encode oncoproteins, cell surface antigens including mols. related to T cell proliferation, transcription factors, and a chemokine receptor. The two downregulated genes encode granzymes that play an important role for induction of cell death. These findings suggest that there is differential gene expression in different clin. phases of T-LGL leukemia and these differentially expressed genes would be potential targets for further studies to identify the genes involved in the transformation process of T-LGL leukemia.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 6 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2004:50309 CAPLUS <<LOGINID::20100206>>
DN 140:156821
TI Expression profiling of the responses of Pneumocystis carinii to drug treatment using DNA macroarrays
AU Collins, Margaret S.; Bansil, Sandeep; Cushion, Melanie T.
CS University of Cincinnati College of Medicine, Cincinnati, OH, 45267, USA
SO Journal of Eukaryotic Microbiology (2003), 50(Suppl.), 605-606 CODEN: JEMIEI; ISSN: 1066-5234
PB Society of Protozoologists
DT Journal
LA English
AB A DNA macroarray anal. was conducted to assess the effects of selected compds. on transcription profiles of Pneumocystitis carinii as a means to better understand the mechanisms of action of these compds. The macroarray technique successfully detected changes in ***expression*** ***profiles*** of P. carinii in response to ***different*** compds. and will be useful for identification of new ***drug*** targets and understanding their mechanisms of action. Organism viability and time of exposure were obsd. to be crit. to gene regulation as many genes initially exhibited up-regulation and later dramatically down-regulation.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 7 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2004:34495 CAPLUS <<LOGINID::20100206>>
DN 140:247328
TI Similarities and differences in uterine gene expression patterns caused by treatment with physiological and non-physiological estrogens
AU Watanabe, H.; Suzuki, A.; Kobayashi, M.; Lubahn, D. B.; Handa, H.; Iguchi, T.
CS Center for Integrative Bioscience, Okazaki National Research Institutes and Core Research for Evolution Science and Technology (CREST), Japan Science and Technology Corporation, Okazaki, 444-8585, Japan
SO Journal of Molecular Endocrinology (2003), 31(3), 487-497 CODEN: JMLEEI; ISSN: 0952-5041
PB Society for Endocrinology
DT Journal
LA English
AB Administration of physiol. and non-physiol. estrogens during pregnancy or after birth is known to have adverse effects on the development of the reproductive tract and other organs. Although it is believed that both estrogens have similar effects on gene expression, this view has not been tested systematically. To compare the effects of physiol. (estradiol; E2) and non-physiol. (diethylstilbestrol; DES) estrogens, we used DNA microarray anal. to examine the uterine gene expression patterns induced by the two estrogens. Although E2 and DES induced many genes to respond in the same way, different groups of genes showed varying levels of maximal activities to each estrogen, resulting in different dose-response patterns. Thus, each estrogen has a distinct effect on uterine gene expression. The genes were classified into clusters according to their dose-responses to the two estrogens. Of the eight clusters, only two correlated well with the uterotropic effect of different doses of E2. One of these clusters contained genes that were upregulated by E2, which included genes encoding several stress proteins and transcription factors. The other cluster contained genes that were downregulated by E2, including genes related to metab., transcription and detoxification processes. The expression of these genes in estrogen receptor-deficient mice was not affected by E2 treatment, indicating that these genes are affected by the E2-bound estrogen receptor. Thus, of the many genes that are affected by estrogen, it was suggested that only a small no. are directly involved in the uterotropic effects of estrogen treatment.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 8 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2004:26318 CAPLUS <<LOGINID::20100206>>
DN 141:17019
TI Transcriptomic classification of antitumor agents: application to the analysis of the antitumoral effect of SR31747A
AU Ferrini, Jean-Bernard; Jbilo, Omar; Peleraux, Annick; Combes, Therese; Vidal, Hubert; Galiegue, Sylvaine: Casellas, Pierre
CS Immunology-Oncology Department, Sanofi-Synthelabo Recherche, Montpellier, F-34184, Fr.
SO Gene Expression (2003), 11(3/4), 125-139 CODEN: GEEXEJ; ISSN: 1052-2166
PB Cognizant Communication Corp.
DT Journal
LA English
AB SR31747A is a sigma ligand that exhibits a potent antitumoral activity on various human tumor cell lines both in vitro and in vivo. To understand its mode of action, we used DNA microarray technol. combined with a new bioinformatic

approach to identify genes that are modulated by SR31747A in different human breast or prostate cancer cell lines. The SR31747A transcriptional signature was also compared with that of seven different representative anticancer drugs commonly used in the clinic. To this aim, we performed a two-dimensional hierarchical clustering anal. of drugs and genes which showed that (1) std. mols. with similar mechanism of action clustered together and (2) SR31747A does not belong to any previously characterized class of std. anticancer drugs. Moreover, we showed that (3) SR31747A mainly exerted its antiproliferative effect by inhibiting the expression of genes playing a key role in DNA replication and cell cycle progression. Finally, contrasting with other drugs, we obtained evidence that (4) SR31747A strongly inhibited the expression of three key enzymes of the nucleotide synthesis pathway (i.e., dihydrofolate reductase, thymidylate synthase, and thymidine kinase) with the latter shown both at the mRNA and protein levels. These results, obtained through a novel mol. approach to characterize and compare anticancer agents, showed that SR31747A exhibits an original mechanism of action, very likely through unexpected targets whose modulations may account for its antitumoral effect.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 76 THERE ARE 76 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 9 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:1008941 CAPLUS <<LOGINID::20100206>>
DN 140:197383
TI Developmental changes in glutathione S-transferase isoforms expression and activity in intrasplenic fetal liver tissue transplants in rats
AU Lupp, Amelie; Anschuetz, Tino; Lindstrom-Seppa, Pirjo; Mueller, Dieter
CS Institute of Pharmacology and Toxicology, Friedrich Schiller University Jena, Jena, Germany
SO Experimental and Toxicologic Pathology (2003), 55(2-3), 107-119 CODEN: ETPAEK; ISSN: 0940-2993
PB Urban & Fischer Verlag GmbH & Co. KG
DT Journal
LA English
AB The aim of the present study was to characterize developmental changes in glutathione S-transferase (GST) isoforms expression and in glutathione conjugation capacity in intrasplenic liver tissue transplants. For this purpose, syngenic fetal liver tissue suspensions were transplanted into the spleens of adult male Fischer 344 rats. Three days, 1, 2, 4 wk, 2, 4, 6 mo and 1 yr later, transplant-recipients and control animals were sacrificed and class .alpha., .mu. and .vpi. GST isoforms expression and GST activities using the substrates o-dinitrobenzene and 1-chloro-2,4-dinitrobenzene were assessed in livers and spleens. In the hepatocytes of the adult livers no class .vpi., but a distinct class .alpha. and .mu. GST expression was seen. The bile duct epithelia were class .vpi. GST pos. Fetal livers displayed almost no class .alpha. and .mu., but a slight class .vpi. GST expression. The same pattern was seen in 3-day-old in trasplenic liver tissue transplants. Up to 2 wk after surgery the class .alpha. and .mu. GST expression increased in the hepatocytes of the transplants, whereas the immunostaining for class .vpi. GST disappeared. No remarkable changes were seen thereafter. Normal conjugation capacities were obsd. with the livers of both groups of rats. Control spleens displayed only low GST activities. From 2 mo after transplantation on activities were significantly higher in transplant-contg. spleens than in resp. control organs with a further increase up to one year after grafting. These results show that intrasplenically transplanted fetal liver cells proliferate and ***differentiate*** into mature cells displaying a GST ***expression*** ***pattern*** with resp. enzyme ***activities*** similar to adult liver.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 10 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:1005539 CAPLUS <<LOGINID::20100206>>
DN 140:210322
TI Gene expression profile revealed different effects of angiotensin II receptor blockade and angiotensin-converting enzyme inhibitor on heart failure
AU Mizukami, Miho; Hasegawa, Hiroshi; Kohro, Takahide; Toko, Haruhiro; Kudoh, Sumiyo; Zou, Yunzeng; Aburatani, Hiroyuki; Komuro, Issei
CS Department of Cardiovascular Science and Medicine, Chiba University Graduate School of Medicine, Chiba, Japan
SO Journal of Cardiovascular Pharmacology (2003), 42(Suppl. 1), S1-S6 CODEN: JCPCDT; ISSN: 0160-2446
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB Although recent clin. studies have indicated that angiotensin II receptor blocker is as effective in treating heart failure as an angiotensin-converting enzyme inhibitor, it is unknown whether their effects are different. Dahl salt-sensitive rats were treated with an angiotensin-converting enzyme inhibitor benazepril, and an angiotensin II receptor blocker candesartan from 11 wk old. We examd. cardiac geometry and function by echocardiog., and histol. and gene expression by high-d. oligonucleotide arrays using Affymetrix U34 (Affymetrix, Santa Clara, CA, U.S.A.). Dahl salt-sensitive rats fed a high salt diet showed a marked increase in blood pressure and developed concentric hypertrophy at 11 wk, followed by left ventricle dilation and congestive heart failure by 20 wk after birth. Although both medications had only a mild antihypertensive effect, they strongly suppressed the development of cardiac hypertrophy, fibrosis and heart failure to the same extent. Gene ***expression*** ***pattern*** examd. by Affymetrix GeneChip (Affymetrix) is quite ***different*** between the two ***drug*** groups, indicating that angiotensin II receptor blocker and angiotensin-converting enzyme inhibitor prevent heart failure by different mechanisms.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 11 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:962499 CAPLUS <<LOGINID::20100206>>
DN 140:318059
TI ILR1 and slLR1 IAA amidohydrolase homologs differ in expression pattern and substrate specificity
AU Campanella, James J.; Ludwig-Mueller, Jutta; Bakllamaja, Vinela; Sharma, Vipul; Cartier, Ania
CS Department of Biology and Molecular Biology, Montclair State University, Montclair, NJ, 07043, USA

SO Plant Growth Regulation (2003), 41(3), 215-223 CODEN: PGRED3; ISSN: 0167-6903
PB Kluwer Academic Publishers
DT Journal
LA English
AB We have recently isolated and characterized a homolog of the Arabidopsis thaliana IAA amidohydrolase ILR1 from Arabidopsis suecica (sILR1). This study examines the enzymic characteristics of sILR1, as well as spatial and temporal expression of sILR1 compared to ILR1. The sILR1 protein can utilize IAA-alanine and IAA-glycine as substrates more effectively than ILR1. In contrast to ILR1, sILR1 cannot cleave IAA-phenylalanine or IAA-leucine as substrates. ILR1 and sILR1 share a pH optimum of 8.0 in Tris buffer. Based on the calcd. Kmax value, sILR1 has a higher affinity for IAA-alanine than ILR1. The sILR1 transcript is first detectable in seedlings at day 4 after germination and rises to a steady state level from day 5 to day 15. In A. thaliana, expression of ILR1 begins with a burst at day 1 and decreases over 15 days to a relatively low, but steady state level. Examn. of ILR1 and sILR1 transcripts in different tissues shows that both sILR1 and ILR1 are highly expressed in roots, although ILR1 appears more highly expressed in hypocotyls, flowers, and basal leaves than sILR1.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 12 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:900297 CAPLUS <<LOGINID::20100206>>
DN 140:25990
TI Rats with low exploratory activity in the elevated plus-maze have the increased expression of limbic system-associated membrane protein gene in the periaqueductal grey
AU Nelovkov, Aleksei; Philips, Mari-Anne; Koks, Sulev; Vasar, Eero
CS Department of Physiology, University of Tartu, Tartu, 50411, Estonia
SO Neuroscience Letters (2003), 352(3), 179-182 CODEN: NELED5; ISSN: 0304-3940
PB Elsevier Science Ltd.
DT Journal
LA English
AB The aim of a present study was to analyze the gene expression profiles in the periaqueductal gray (PAG) of rats related to their exploratory activity in the elevated plus-maze model of anxiety. Animals were divided into the groups according to their exploratory activity in the plus-maze as follows: rats with low activity ('anxious'), moderate activity ('intermediate') and high activity ('non-anxious'). Control animals were not exposed to the elevated plus-maze. The differential expression of genes was analyzed using the cDNA representational difference anal. (RDA) in combination with the sequencing and database search. Reverse transcription-polymerase chain reaction with specific primers was applied to confirm the differences found by the RDA. We established that animals displaying the ***different*** exploratory ***activity*** have also the ***different*** gene ***expression*** ***profiles*** in the PAG. Among the identified genes, we were able to confirm the increased expression of limbic system-assocd. membrane protein (LSAMP) in animals having the reduced exploratory activity in the elevated plus-maze. Anxious' group of rats had 1.6-fold higher expression of LSAMP gene compared to non-anxious' animals. By contrast, home-cage' control rats and intermediate' group did not differ significantly by their LSAMP gene expression level. In conclusion, it is likely that LSAMP plays a role in the regulation of exploratory behavior of rats in the novel aversive environment.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 13 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:900153 CAPLUS <<LOGINID::20100206>>
DN 140:92389
TI Quantitative and qualitative ***changes*** in gene ***expression*** ***patterns*** characterize the ***activity*** of plaques in multiple sclerosis
AU Tajouri, Lotti; Mellick, Albert S.; Ashton, Kevin J.; Tannenberg, Anthony E. G.; Nagra, Rashed M.; Tourtellotte, Wallace W.; Griffiths, Lyn R.
CS School of Health Science, Griffith University, Southport, QLD 4215, Australia
SO Molecular Brain Research (2003), 119(2), 170-183 CODEN: MBREE4; ISSN: 0169-328X
PB Elsevier Science B.V.
DT Journal
LA English
AB Multiple sclerosis (MS) is a complex autoimmune disorder of the CNS with both genetic and environmental contributing factors. Clin. symptoms are broadly characterized by initial onset, and progressive debilitating neurol. impairment. In this study, RNA from MS chronic active and MS acute lesions was extd., and compared with patient matched normal white matter by fluorescent cDNA microarray hybridization anal. This resulted in the identification of 139 genes that were differentially regulated in MS plaque tissue compared to normal tissue. Of these, 69 genes showed a common pattern of expression in the chronic active and acute plaque tissues investigated (Pvalue<0.0001, .rho.=0.73, by Spearman's .rho. anal.); while 70 transcripts were uniquely differentially expressed (.gtoreq.1.5-fold) in either acute or chronic active tissues. These results included known markers of MS such as the myelin basic protein (MBP) and glutathione S-transferase (GST) M1, nerve growth factors, such as nerve injury-induced protein 1 (NINJ1), X-ray and excision DNA repair factors (XRCC9 and ERCC5) and X-linked genes such as the ribosomal protein, RPS4X. Primers were then designed for seven array-selected genes, including transferrin (TF), superoxide dismutase 1 (SOD1), glutathione peroxidase 1 (GPX1), GSTP1, crystallin, alpha-B (CRYAB), phosphomannomutase 1 (PMM1) and tubulin .beta.-5 (TBB5), and real time quant. (Q)-PCR anal. was performed. The results of comparative Q-PCR anal. correlated significantly with those obtained by array anal. (r=0.75, Pvalue<0.01, by Pearson's bivariate correlation). Both chronic active and acute plaques shared the majority of factors identified suggesting that quant., rather than gross qual. ***differences*** in gene ***expression*** ***pattern*** may define the progression from acute to chronic ***active*** plaques in MS.
OSC.G 37 THERE ARE 37 CAPLUS RECORDS THAT CITE THIS RECORD (38 CITINGS)
RE.CNT 85 THERE ARE 85 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 14 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2003:875440 CAPLUS <<LOGINID::20100206>>
DN 139:333087
TI Gene expression profile-based method for evaluating a therapeutic potential of a chemical entity
IN Jensen, Jens Bitsch; Hummel, Rene; Mikkelsen, Jens Damsgaard
PA Azign Bioscience A/S, Den.
SO PCT Int. Appl., 40 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003091450 A1 20031106 WO 2003-DK256 20030415
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
AU 2003226947 A1 20031110 AU 2003-226947 20030415
PRAI DK 2002-617 A 20020424 WO 2003-DK256 W 20030415
AB The invention discloses methods for predicting a therapeutic potential of a chem. entity and a specific differential display array. The methodol. of the invention employs gene expression profiles for the chem. entity of interest as well as for a plurality of ref. compds. (e.g. antidepressants and antipsychotics).
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 15 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:863445 CAPLUS <<LOGINID::20100206>>
DN 139:345890
TI Screening of vasodilators with different mode of action based on gene expression profile analysis in vascular smooth muscle cells
IN Tanaka, Toshio; Nishimura, Yuhei; Oda, Naozumi; Ono, Takeshi; Kikuchi, Kaoru; Kimura, Toru
PA Asahi Kasei Corporation, Japan; Sumitomo Pharmaceuticals Co., Ltd.
SO Jpn. Kokai Tokkyo Koho, 98 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI JP 2003310272 A 20031105 JP 2002-126514 20020426
PRAI JP 2002-126514 20020426
AB Methods for screening of vasodilators based on expression profiles of genes responsive to different types of known vasodilators having different mechanism of action, is disclosed. Test compds. are brought into contact with vascular smooth muscle cells and those causing changes in expression level of particular genes found to be responsive to vasodilators are selected. Antihypertensive agents contg. the selected compds. from screening are claimed. Genes whose expression level was significantly altered (> 2 fold or < 50%) in response to vasodilators, hydralazine and prostaglandin E1 were identified in human vascular smooth muscle cell line. Genes responsive to vasoconstrictor angiotensin II, calcium antagonist nifedipine and verapamil hydrochloride, or angiotensin converting enzyme (ACE) inhibitor captopril, were also found independently.

L12 ANSWER 16 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:850152 CAPLUS <<LOGINID::20100206>>
DN 140:56770
TI ***Differential*** ***activities*** , subcellular distribution and tissue ***expression*** ***patterns*** of three members of slingshot family phosphatases that dephosphorylate cofilin
AU Ohta, Yusaku; Kousaka, Kazuyoshi; Nagata-Ohashi, Kyoko; Ohashi, Kazumasa; Muramoto, Aya; Shima, Yasuyuki; Niwa, Ryusuke; Uemura, Tadashi; Mizuno, Kensaku
CS Department of Biomolecular Sciences, Graduate School of Life Sciences, Tohoku University, Miyagi, Japan
SO Genes to Cells (2003), 8(10), 811-824 CODEN: GECERL; ISSN: 1356-9597
PB Blackwell Publishing Ltd.
DT Journal
LA English
AB Cofilin, a key regulator of actin filament dynamics, is inactivated by phosphorylation at Ser-3 by LIM-kinases and is reactivated by dephosphorylation by a family of protein phosphatases, termed Slingshot (SSH). We have identified two novel isoforms of SSHs, termed SSH-2L and SSH-3L and characterized them in comparison with SSH-1L that was previously reported. SSH-1L and SSH-2L, but not SSH-3L, tightly bound to and co-localized with actin filaments. When expressed in cultured cells, SSH-1L, SSH-2L and SSH-3L decreased the level of Ser-3-phosphorylated cofilin (P-cofilin) in cells and suppressed LIM-kinase-induced actin reorganization, although SSH-3L was less effective than SSH-1L and SSH-2L. In cell-free assays, SSH-1L and SSH-2L efficiently dephosphorylated P-cofilin, whereas SSH-3L did do so only weakly. Using deleted mutants of SSH-1L and SSH-2L, we found that the N-terminal and C-terminal extracatalytic regions are crit. for cofilin-phosphatase and F-actin-binding activities, resp. In situ hybridization analyses revealed characteristic patterns of expression of each of the mouse Ssh genes in both neuronal and non-neuronal tissues; in particular, expression of Ssh-3 in epithelial tissues is evident. SSH-1L, SSH-2L and SSH-3L have the potential to dephosphorylate P-cofilin, but subcellular distribution, F-actin-binding ***activity*** , specific phosphatase ***activity*** and ***expression*** ***patterns*** significantly ***differ*** , which suggests that they have related but distinct functions in various cellular and developmental events.
OSC.G 40 THERE ARE 40 CAPLUS RECORDS THAT CITE THIS RECORD (40 CITINGS)
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 17 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:838979 CAPLUS <<LOGINID::20100206>>
DN 140:285674
TI The obesity phenotype and ageing connection in genetically altered FORKO mice
AU Sairam, M. Ram; Wang, Min; Danilovich, Natalia; Xing, Weirong

CS Molecular Reproduction Research Laboratory, Clinical Research Institute of Montreal, Montreal, QC, H2W 1R7, Can.
SO Progress in Obesity Research (2003), 9, 842-847 CODEN: POBREJ; ISSN: 0962-7936
PB John Libbey & Co. Ltd.
DT Journal
LA English
AB The obesity phenotype that appears in genetically modified female and male mice in which the receptor for the glycoprotein hormone FSH (follitropin) has been deleted by homologous recombination. The null females are sterile due to failure of ovulation. Due to estrogen deficiency, they develop various disorders that typify the postmenopausal state in women including obesity, kyphosis, ovarian tumors as well as changes in the central and peripheral nervous systems. The FSH receptor (FSH-R) is a major signaling system in the ovary that is expressed exclusively in granulosa cells of the follicle that contribute to estrogen prodn. during each reproductive cycle. The major changes occur in the adipose tissue in null females and show how the lipid abnormalities may be cor. by estrogen replacement therapy. Using the FORKO model there is an excellent opportunity for exploring the genomic and ***proteomic*** profiles of adipose tissue at ***different*** stages of obesity aiding the discovery of novel ***therapeutic*** measures including non-hormonal agents that are selectively targeted to the adipocyte.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 18 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:837241 CAPLUS <<LOGINID::20100206>>
DN 139:345904
TI Pre-and post therapy gene expression profiling to identify drug targets for treatment of acute lymphoblastic leukemia
IN Evans, William Edward; Relling, Mary V.
PA St. Jude Children's Research Hospital, USA
SO PCT Int. Appl., 66 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003087315 A2 20031023 WO 2003-US10603 20030407 WO 2003087315 A3 20031231 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 20030224422 A1 20031204 US 2003-407790 20030404 AU 2003262185 A1 20031027 AU 2003-262185 20030407
PRAI US 2002-370835P P 20020408 US 2003-449893P P 20030225 WO 2003-US10603 W 20030407
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB This invention presents pre-and post therapy gene expression profiling to identify drug targets for treatment of childhood acute lymphoblastic leukemia (ALL). A general method for identifying biol. targets for improving currently available therapies is provided. Target genes and their expression products are identified based on their response to methotrexate or mercaptopurine therapy as detd. through pre- and post-therapy expression profiles. In another aspect, differences in expression profiles between responsive and nonresponsive patients are taken into account to identify potential new targets for the development of novel medications or treatments. The invention also provides methods for comparing therapies to predict which will have the best therapeutic efficacy and/or the least potential deleterious. The methods taught are specifically applied to identify targets for improving treatment of acute lymphoblastic leukemia.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 19 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:832878 CAPLUS <<LOGINID::20100206>>
DN 140:354578
TI Gene expression profile unravels significant differences between childhood and adult Ph+ acute lymphoblastic leukemia
AU Scrideli, C. A.; Cazzaniga, G.; Fazio, G.; Pirola, L.; Callegaro, A.; Bassan, R.; Rambaldi, A.; Nigro, L. Lo; Basso, G.; Masera, G.; Biondi, A.
CS Ospedale San Gerardo, Centro Ricerca M. Tettamanti, Clinica Pediatrica Universita di Milano-Bicocca, Monza, 224, Italy
SO Leukemia (2003), 17(11), 2234-2237 CODEN: LEUKEI; ISSN: 0887-6924
PB Nature Publishing Group
DT Journal
LA English
AB The expression levels at diagnosis of a selected no. of genes that had emerged as being particularly significant from the two Ph+ gene expression studies were studied to dissect the heterogeneity in Ph+ acute leukemia. Among the 10 genes whose expression was specific enough to discriminate childhood Ph+ leukemia from other genetic subclasses, four related genes were selected: mitogen-activated protein-kinase-activated protein kinase 3, cyclin D2, caspase 8 and caspase 10. A further five genes: histone-deacetylase 2, minichromosome maintenance, S. pombe, homolog of 6, microtubule affinity-regulating kinase 3, beclin 1 and telomerase protein component, were selected from those that presented the highest different ratio of expression in adult Ph+ acute lymphoblastic leukemia (ALL) resistant or sensitive to the tyrosine-kinase inhibitor ST1571. Bone marrow (BM) sample from 26 children and nine adults with Ph + ALL; BM- and PB-mononuclear cells (MNC) from eight and five healthy volunteers, resp. were also studied. The panel of selected genes whose expression is significantly different in normal BM and Ph + ALL could suggest a possible participation of some of these genes in the Ph + leukemogenic process. A significant difference in gene expression profile between adult and children Ph + ALL was found; suggesting that childhood Ph + ALL is a heterogeneous disease also at biol. level. However, no distinct pattern within childhood Ph + ALL was identified according to steroid response.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 20 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:808528 CAPLUS <<LOGINID::20100206>>
DN 140:157781
TI Changes in hippocampal gene expression after neuroprotective activation of group I metabotropic glutamate receptors
AU Blaabjerg, Morten; Baskys, Andrius; Zimmer, Jens; Vawter, Marquis P.
CS Anatomy and Neurobiology, University of Southern Denmark, Odense, Den.
SO Molecular Brain Research (2003), 117(2), 196-205 CODEN: MBREE4; ISSN: 0169-328X
PB Elsevier Science B.V.
DT Journal
LA English
AB Stimulation of group I metabotropic glutamate receptors (mGluRs) has been shown to protect against N-methyl-d-aspartate receptor-mediated cell death, but the underlying cellular mechanism is unknown. Using cDNA microarrays the authors have now compared gene expressions in organotypic hippocampal slice cultures after neuroprotective activation of group I mGluRs with (S)-3,5-dihydroxyphenylglycine (DHPG; 10 .mu.M, 2 h) with untreated control cultures. Total RNA was extd. from the cultures immediately after the neuroprotective treatment, reverse transcribed to cDNA with incorporation of [32]P-dCTP, and then hybridized to the arrays. Of a total of 1128 genes on the Neuroarray, 33 genes displayed significant changes in expression after DHPG-treatment (six up- and 27 downregulated). These genes have been assocd. with regulation of synaptic excitation, inflammation, cell adhesion, cell death, and transcription. The small GTPase RAB5B assocd. with endocytosis emerged as a primary candidate gene for neuroprotection, and its expression was confirmed by Western blot anal. and real time polymerase chain reaction. By providing insight into genes involved in neuroprotection these data may help to identify novel therapeutic targets.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 21 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:796220 CAPLUS <<LOGINID::20100206>>
DN 139:287366
TI Genes differentially expressed in prostate cancer and their diagnostic and therapeutic uses
IN Faris, Mary; Pearson, Cecelia I.
PA USA
SO U.S. Pat. Appl. Publ., 42 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 20030190640 A1 20031009 US 2002-252157 20020529
PRAI US 2001-295048P P 20010531
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The present invention relates to a combination comprising a plurality of cDNAs which are differentially expressed in prostate cancer and which may be used in their entirety or in part as to diagnose, to stage to treat or to monitor the progression or treatment of prostate cancer. Thus, 501 cDNAs are identified that are either down-regulated or up-regulated in prostate cancer cells in comparison to normal prostate tissues. Hybridization detection of the cDNA levels are diagnostic for prostate cancer, and screening assays are provided for ligands that bind either the cDNA or the protein products.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L12 ANSWER 22 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:765977 CAPLUS <<LOGINID::20100206>>
DN 140:56577
TI Activation of hypersensitive response genes in the absence of pathogens in transgenic tobacco plants expressing a rice small GTPase
AU Yoda, Hiroshi; Sano, Hiroshi
CS Research and Education Center for Genetic Information, Nara Institute of Science and Technology, Nara, 630-0192, Japan
SO Planta (2003), 217(6), 993-997 CODEN: PLANAB; ISSN: 0032-0935
PB Springer-Verlag
DT Journal
LA English
AB Transgenic tobacco (Nicotiana tabacum L.) plants constitutively expressing a rice (Oryza sativa L.) gene encoding a small GTPase, rgp1, showed marked resistance to tobacco mosaic virus (TMV) infection compared with the wild type [H. Sano et al. (1994) Proc Natl Acad Sci USA 91:10556-10560]. To examine the gene ***expression*** ***profile*** , the temp.- ***shift*** method was adopted to hyper-***activate*** the N-gene inducing the hypersensitive response (HR), and transcripts of 11 representative HR genes were analyzed. In transgenic and wild-type plants, transcripts of 10 genes were induced during the HR; however, in most cases, their expression level was higher in the former than in the latter. Mock treatment of transgenic plants also efficiently induced transcripts of 8 out of 11 genes after temp. shift, indicating that their activation is mediated by the N-gene. Salicylic acid and its glucoside-conjugates were induced in both transgenic and wild-type plants, but their quantity in the former was unusually higher than in the latter. These results suggest that expression of rgp1 pos. influenced the signaling pathway of the HR, resulting in higher induction of salicylates. This possibly caused a "priming effect" that hyper-activates the HR genes through the N-gene without TMV infection. It was thus conceivable that, despite a structural similarity to the Rab-family of GTPases, which function in membrane trafficking, rgp1 might participate in the signal transduction pathway of the HR.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 23 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:760852 CAPLUS <<LOGINID::20100206>>
DN 139:304730
TI Multiple corticosteroid receptors in a teleost fish: distinct sequences, expression patterns, and transcriptional activities
AU Greenwood, Anna K.; Butler, Paul C.; White, Richard B.; DeMarco, Ulrike; Pearce, David; Fernald, Russell D.
CS Program in Neuroscience, Stanford University, Stanford, CA, 94305-2130, USA

SO Endocrinology (2003), 144(10), 4226-4236 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB We describe the characterization of 4 corticosteroid receptors (CRs) in a cichlid fish, Haplochromis burtoni: a previously undescribed glucocorticoid receptor (GR) (HbGR1), another GR expressed in 2 splice isoforms (HbGR2a and HbGR2b), and an mineralocorticoid receptor (MR) (HbMR). Sequence comparison and phylogenetic anal. showed that these CRs sort naturally into GR and MR groups, and that the GR duplication we describe will probably be common to all teleosts. Quant. PCR revealed differential patterns of CR tissue expression in organs dependent on corticosteroid action. Trans-activation assays demonstrated that the CRs were selective for corticosteroid hormones and showed that the HbMR was similar to mammalian MRs in being more sensitive to both cortisol and aldosterone than the GRs. Addnl., the 2 HbGR2 isoforms were expressed uniquely in different tissues and were functionally distinct in their actions on classical GR-sensitive promoters. The identification of four CR subtypes in teleosts suggests a more complicated corticosteroid signaling in fish than previously recognized.
OSC.G 74 THERE ARE 74 CAPLUS RECORDS THAT CITE THIS RECORD (74 CITINGS)
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 24 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:742498 CAPLUS <<LOGINID::20100206>>
DN 140:40152
TI Different CREM-isoform gene expression between equine and human normal and impaired spermatogenesis
AU Blocher, Sonja; Behr, Rudiger; Weinbauer, Gerhard F.; Bergmann, Martin; Steger, Klaus
CS Institute of Veterinary Anatomy, Histology and Embryology, University of Giessen, Giessen, 35392, Germany
SO Theriogenology (2003), 60(7), 1357-1369 CODEN: THGNBO; ISSN: 0093-691X
PB Elsevier Science Inc.
DT Journal
LA English
AB Histone-to-protamine exchange causes chromatin condensation ceasing gene expression in elongating spermatids. Gene expression of protamines is regulated by the transcription factor cAMP-responsive element modulator (CREM). Altered CREM expression results in male infertility, as shown by CREM-knock-out mice being sterile due to round spermatid maturation arrest and patients exhibiting round spermatid maturation arrest revealing a lack or substantial redn. of both CREM-mRNA and CREM-protein. Similar defects in histone-to-protamine exchange have been suggested in infertile stallions exhibiting enlarged sperm heads. The CREM-gene consists of 14 exons. Alternative exon splicing results in the prodn. of both activator and repressor proteins. To further clarify the role of different CREM-isoforms for male infertility, the expression pattern of various CREM-isoforms during equine and human normal and impaired spermatogenesis was investigated by RT-PCR. Stallions with normal spermatogenesis expressed six activators and three repressors. In men three activators and seven different repressors were detected. In one stallion and patients with impaired spermatogenesis, only repressors were found. It is concluded that (i) stallion and man reveal a ***different*** CREM ***expression*** ***pattern*** , (ii) the expression of CREM ***activators*** is a prerequisite for normal spermatogenesis, and (iii) the lack of CREM activator expression results in male infertility.
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 25 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:738388 CAPLUS <<LOGINID::20100206>>
DN 140:285045
TI Pilot study on changes of gene expression profiles and interaction of genes in cardiac hypertrophy
AU Zhang, Youyi; Han, Qide
CS Third Hospital, Peking University, Beijing, 100083, Peop. Rep. China
SO Beijing Daxue Xuebao, Yixueban (2002), 34(5), 585-589 CODEN: BDXYAH; ISSN: 1671-167X
PB Beijing Daxue
DT Journal; General Review
LA Chinese
AB A review. Gene expression profiles, obtained with DNA microarray (cDNA or oligonucleotide), will provide the basis for understanding how genes work together to guide the functions of cells. In order to discover gene expression changes related to distinct cardiac hypertrophy status, myocardial gene expression profile from different cardiac hypertrophy models were examd. by cDNA microarray in our study. Those changed genes were clustered to several groups, in each of which genes acted in similar expression behavior. We intend to provide insight into the interaction of genes and explore the research strategy for the complex system.

L12 ANSWER 26 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:712740 CAPLUS <<LOGINID::20100206>>
DN 140:121792
TI Paradigm shift of integrated drug discovery
AU Noguchi, Teruaki
CS Tenox Research Institute, Japan
SO Jisedai Genomu Soyaku (2003), 1-5. Editor(s): Sugiyama, Yuichi. Publisher: Nakayama Shoten, Tokyo, Japan. CODEN: 69EMCR; ISBN: 4-521-01551-4
DT Conference; General Review
LA Japanese
AB A review, discussing paradigm shift of integrated genomic drug discovery with regards to drug design by pharmacoproteomics, QSAR, and mol. targeting.

L12 ANSWER 27 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:701330 CAPLUS <<LOGINID::20100206>>
DN 139:306350
TI Rheumatoid arthritis is a heterogeneous disease: Evidence for differences in the activation of the STAT-1 pathway between rheumatoid tissues
AU van der Pouw Kraan, Tineke C. T. M.; van Gaalen, Floris A.; Kasperkovitz, Ria V.; Verbeet, Nicolette L.; Smeets, Tom J. M.; Kraan, Maarten C.; Fero, Mike; Tak, Paul-Peter; Huizinga, Tom W. J.; Pieterman, Elsbet; Breedveld, Ferdinand C.; Alizadeh, Ash A.; Verweij, Cornelis L.
CS VU Medical Center, Amsterdam, Neth.

SO Arthritis & Rheumatism (2003), 48(8), 2132-2145 CODEN: ARHEAW; ISSN: 0004-3591
PB John Wiley & Sons, Inc.
DT Journal
LA English
AB Objective. To generate a mol. description of synovial tissue from rheumatoid arthritis (RA) patients that would allow us to unravel novel aspects of pathogenesis and to identify different forms of disease. Methods. We applied complementary DNA microarray anal. to profile gene expression, with a focus on immune-related genes, in affected joint tissues from RA patients and in tissues from osteoarthritis (OA) patients as a control. To validate microarray data, real-time polymerase chain reaction was performed on genes of interest. Results. The gene expression signatures of synovial tissues from RA patients showed considerable variability, resulting in the identification of at least two molecularly distinct forms of RA tissues. One class of tissues revealed abundant expression of clusters of genes indicative of an involvement of the adaptive immune response. Detailed anal. of the expression profile provided evidence for a prominent role of an activated signal transducer and activator of transcription 1 pathway in these tissues. The expression profiles of another group of RA tissues revealed an increased tissue remodeling activity and a low inflammatory gene expression signature. The gene expression pattern in the latter tissues was reminiscent of that obsd. in the majority of OA tissues. Conclusion. The differences in the gene expression profiles provide a unique perspective for distinguishing different pathogenetic RA subsets based on mol. criteria. These data reflect important aspects of mol. variation that are relevant for understanding the biol. dysregulation underlying these subsets of RA. This approach may also help to define homogeneous groups for clin. studies and evaluation of targeted therapies.
OSC.G 49 THERE ARE 49 CAPLUS RECORDS THAT CITE THIS RECORD (49 CITINGS)
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 28 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:697939 CAPLUS <<LOGINID::20100206>>
DN 139:257661
TI Proteomic changes in renal cancer and co-ordinate demonstration of both the glycolytic and mitochondrial aspects of the Warburg effect
AU Unwin, Richard D.; Craven, Rachel A.; Harnden, Patricia; Hanrahan, Sarah; Totty, Nick; Knowles, Margaret; Eardley, Ian; Selby, Peter J.; Banks, Rosamonde E.
CS Cancer Research UK, Clinical Unit, St. James's University Hospital, Leeds, UK
SO Proteomics (2003), 3(8), 1620-1632 CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
AB Renal cell carcinoma (RCC) is the tenth most common cancer although the incidence is increasing. The main clin. problems stem from the relatively late presentation of many patients due to the often asymptomatic nature of the illness, and the relative insensitivity of metastatic disease to conventional chemotherapy and radiotherapy. Despite increasing knowledge of some of the genetic changes underlying sporadic renal cancer such as those involving the Von Hippel Lindau (VHL) gene, many of the underlying pathophysiol. changes are ill-defined and there remains a need for the identification of disease markers for use in diagnosis and prognosis or as potential therapeutic targets. This study has used a proteomic approach, based on two-dimensional gel electrophoresis and mass spectrometry, to compare the protein profiles of conventional RCC tissue with patient-matched normal kidney cortex. Sequencing of 32 protein spots with significantly increased expression in RCC samples (.gtoreq. 4/6 patients) and 41 proteins whose levels decreased (6/6 patients) confirmed several previously known RCC-associd. changes such as increases in Mn-superoxide dismutase, lactate dehydrogenase-A, aldolase A and C, pyruvate kinase M2, and thymidine phosphorylase. Addnl., several previously unknown changes were identified, including increased expression of three members of the annexin family and increased levels of the actin depolymn. factor cofilin. The Warburg effect was also demonstrated with the identification of increases in proteins involved in the majority of steps in the glycolytic pathway and decreases in the gluconeogenic reactions, together with a parallel decrease in several mitochondrial enzymes. A no. of the alterations seen were further confirmed in addnl. samples by immunohistochem., Western blotting, and laser capture microdissection.
OSC.G 82 THERE ARE 82 CAPLUS RECORDS THAT CITE THIS RECORD (82 CITINGS)
RE.CNT 82 THERE ARE 82 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 29 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:695226 CAPLUS <<LOGINID::20100206>>
DN 139:378910
TI The essential similarity of TGF.beta. and activin receptor transcriptional responses in cancer cells
AU Ryu, Byungwoo; Kern, Scott E.
CS Sidney Kimmel Comprehensive Cancer Center and Department of Oncology, The Johns Hopkins Medical Institutions, Baltimore, MD, USA
SO Cancer Biology & Therapy (2003), 2(2), 164-170 CODEN: CBTAAO; ISSN: 1538-4047
PB Landes Bioscience
DT Journal
LA English
AB The binding of activin and TGF.beta. to their resp. receptors initiates signals that are carried by common intermediates (Smad proteins) to induce transcriptional activation of downstream genes. Mutations in tumors indicate that both receptor types convey tumor-suppressive signals, among other biol. roles, but their resp. sets of transcriptional targets (transcriptomes) and the shared degree of transcriptome similarity are not well explored in these cells. Transcriptome ***changes*** were analyzed by gene ***expression*** ***profiling*** after expression of constitutively ***active*** ***activin*** type I (ALK4m) and TGF.beta. type I (ALK5m) receptors and by variation of Smad4 expression in cancer cells. Eleven of 15 previously reported TGF.beta. downstream genes were confirmed to be responsive to TGFb and activin receptors in cancer cells. Expression profiling detected eight of these 11, as well as 13 new Smad4-dependent transcripts. Although Smad4-dependent CDKN1A/p21 induction represents the sole known effector of TGF.beta. and activin tumor-suppressor effects, many downstream genes have not yet been evaluated for a suppressive role. A high similarity of TGF.beta. and activin responses among the known and new transcriptional target genes indicated an essential redundancy of the two related inputs. This similarity helps relate the mutations seen in both receptor systems and their Smad mediators in human cancers.

OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 30 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:691703 CAPLUS <<LOGINID::20100206>>
DN 139:290112
TI Variation in gene expression patterns in human gastric cancers
AU Chen, Xin; Leung, Suet Y.; Yuen, Siu T.; Chu, Kent-Man; Ji, Jiafu; Li, Rui; Chan, Annie S. Y.; Law, Simon; Troyanskaya, Olga G.; Wong, John; So, Samuel; Botstein, David; Brown, Patrick O.
CS Department of Surgery, Stanford University School of Medicine, Stanford, CA, 94305, USA
SO Molecular Biology of the Cell (2003), 14(8), 3208-3215
CODEN: MBCEEV; ISSN: 1059-1524
PB American Society for Cell Biology
DT Journal
LA English
AB Gastric cancer is the world's second most common cause of cancer death. The authors analyzed gene expression patterns in 90 primary gastric cancers, 14 metastatic gastric cancers, and 22 nonneoplastic gastric tissues, using cDNA microarrays representing .apprx.30,300 genes. Gastric cancers were distinguished from nonneoplastic gastric tissues by characteristic differences in their gene expression patterns. The authors found a diversity of gene expression patterns in gastric cancer, reflecting variation in intrinsic properties of tumor and normal cells and variation in the cellular compn. of these complex tissues. The authors identified several genes whose expression levels were significantly correlated with patient survival. The variations in gene ***expression*** ***patterns*** among cancers in ***different*** patients suggest ***differences*** in pathogenetic pathways and potential ***therapeutic*** strategies.
OSC.G 68 THERE ARE 68 CAPLUS RECORDS THAT CITE THIS RECORD (68 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 31 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:679512 CAPLUS <<LOGINID::20100206>>
DN 139:275347
TI Transforming growth factor-.beta. as a regulator of site-specific T-cell inflammatory response
AU Luoviksson, B. R.; Gunnlaugsdottir, B.
CS Institute of Laboratory Medicine, Department of Immunology, Landspitali-University Hospital, Reykjavik, Iceland
SO Scandinavian Journal of Immunology (2003), 58(2), 129-138
CODEN: SJIMAX; ISSN: 0300-9475
PB Blackwell Publishing Ltd.
DT Journal; General Review
LA English
AB A review. A common immunopathol. hallmark of many autoimmune inflammatory diseases is a T-cell invasion and accumulation at the inflamed tissue. Although the exact mol. and microenvironmental mechanisms governing such cellular invasion and tissue retention are not known, some key immunol. principles must be at work. Transforming growth factor-.beta. (TGF-.beta.) is known to modulate some of these processes including homing, cellular adhesion, chemotaxis and finally T-cell activation, differentiation, and apoptosis. The chronicity of such T-cell-driven inflammation probably involves an innate immunol. response leading to a T-1 (Th/Tc), T-2, or T-3 (Th/Tr) T-cell adaptive immune response. Several studies suggest that the key to T-cell final destination resides on its and the antigen-presenting cell's phenotype as well as the coreceptor expression pattern and their signaling intensity. Recent observations suggest other equally important regulatory elements of T-cell inflammatory response that are sensitive to TGF-.beta. modulation. These include: (1) the stage of T-cell ***activation*** / ***differentiation*** ; (2) the chemotactic/adhesion mol. ***expression*** ***pattern*** ; and (3) the conditioning at the immunol. synapse detg. their sensitivity to known regulators such as TGF-.beta.. Here, the authors focus on how the phenotype of the responding T cell and the T-cell receptor (TCR)-signaling intensity could drive the given inflammatory response. In particular, they discuss how TGF-.beta. can influence the process of T-cell migration and activation during such site-specific inflammation.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 106 THERE ARE 106 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 32 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:656871 CAPLUS <<LOGINID::20100206>>
DN 139:192783
TI Microarray gene expression profiles of rat tissues exposed to cardiotoxins, identification of toxicity markers and uses for drug screening and modeling toxicity of unknown compounds
IN Mendrick, Donna; Porter, Mark; Johnson, Kory; Higgs, Brandon; Castle, Arthur; Blashoff, Michael
PA Gene Logic, Inc., USA
SO PCT Int. Appl., 209 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 4 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003068908 A2 20030821 WO 2002-US21735 20020710
WO 2003068908 A3 20040226
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG CA 2452897 A1 20030821 CA 2002-2452897 20020710 AU 2002365904 A1 20030904 AU 2002-365904 20020710 EP 1412537 A2 20040428 EP 2002-806804 20020710 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK JP 2005517400 T 20050616 JP 2003-568023 20020710
PRAI US 2001-303819P P 20010710 US 2001-305623P P 20010717 US 2002-369351P P 20020403 US 2002-377611P P 20020506 WO 2002-US21735 W 20020710

AB The present invention presents methods of predicting and modeling toxic effects, the progression of toxic effects and, in specific, the cardiotoxicity of a compd. It includes methods of identifying agents that modulate the onset or progression of a toxic response, predicting the cellular pathways that a compd. modulates, and identifying agents that modulate protein activities. To evaluate and identify gene expression changes that are predictive of toxicity, studies using selected compds. with well-characterized cardiotoxicity were conducted to catalog altered gene expression profiles during exposure in vivo and in vitro. Cyclophosphamide, ifosfamide, minoxidil, hydralazine, BI-QT, clenbuterol, isoproterenol, norepinephrine, and epinephrine were selected as known cardiotoxins. This invention is based on the elucidation of the global changes in gene expression and the identification of toxicity markers in tissues or cells exposed to these cardiotoxins. The toxicity markers may be used in drug screening and toxicity assays. The invention includes a database of rat genes, characterized by toxin-induced differential expression, that is designed for use with microarrays and other solid-phase probes. Examples are presented using gene expression data to model sample toxicity.

L12 ANSWER 33 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:639697 CAPLUS <<LOGINID::20100206>>
DN 140:138962
TI Microarray-based gene expression profiles of allograft rejection and immunosuppression in the rat heart transplantation model
AU Erickson, Laurie M.; Pan, Fan; Ebbs, Aaron; Kobayashi, Masakazu; Jiang, Hongsi
CS Fujisawa Research Institute of America, Northwestern University/Evanston Research Park, Evanston, IL, USA
SO Transplantation (2003), 76(3), 582-588 CODEN: TRPLAU; ISSN: 0041-1337
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB BACKGROUND: Gene expression profiling has the potential to produce new insights into complex biol. systems. To test the value of complement DNA arrays in identifying pathways involved in organ transplant rejection, we examd. the gene expression profiles of rat heart allografts from recipients treated with or without immunosuppression to prevent acute allograft rejection. METHODS: Heterotopic heart transplantation was performed using ACI or Lewis donors and Lewis recipients. Recipients were treated with tacrolimus (Tac) or cyclosporine (CsA) at the equiv. EDs, and graft hearts were harvested on days 3, 5, and 7. A com. microarray was used to measure gene expression levels of 588 genes in day 5 grafts. Selected genes were analyzed by reverse transcriptase-polymerase chain reaction. RESULTS: The expression levels of 118 genes were perturbed in the untreated allograft in comparison with the isograft control, of which 77 genes were categorized as candidate genes for Tac- or CsA-mediated immunosuppression or both, and 41 as genes assocd. with other pathways. Among the 77 candidate genes, 55 genes shared the same response to suppression by both drugs, including inducible nitric oxide synthase, interferon-gamma., and interferon regulatory factor 1. Drug-specific effects were obsd. in 22 genes: Fourteen genes were exclusively reversed by Tac and eight by CsA. CONCLUSIONS: Gene expression profiling reveals a large variety of genes affected during acute rejection, indicating that multiple metabolic pathways, including immune and nonimmune responses, are involved in the local graft rejection events. The ***differences*** and similarities of the gene ***expression*** ***profiles*** relative to the two immunosuppressants may provide more detailed ***therapeutic*** approaches for optimal immunosuppression.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 34 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:633171 CAPLUS <<LOGINID::20100206>>
DN 139:160778
TI Frontal cortex and/or cerebellum differentially expressed genes, psychiatric disorder-associated genes, and diagnostic and therapeutic uses
IN Sklar, Pamela; Petryshen, Tracey; Tsan, Gloria; Lehar, Joseph
PA Whitehead Institute for Biomedical Research, USA
SO U.S. Pat. Appl. Publ., 22 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ---------- --------
PI US 20030152972 A1 20030814 US 2002-292382 20021108
PRAI US 2001-348028P P 20011108
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The disclosure relates to methods of diagnosing psychiatric disorders (e.g., schizophrenia, bipolar disorder), methods of classifying a sample as derived from an individual having a psychiatric disorder, methods of identifying compds. for use in modulating psychiatric disorders, methods of modulating psychiatric disorders and methods of assessing efficacy of treatment of psychiatric disorders. The disclosure also relates to oligonucleotide microarrays contg. probes for genes which are differentially expressed between schizophrenic individuals and normal individuals and to oligonucleotide microarrays contg. probes for genes which are differentially expressed between bipolar individuals and normal individuals. The disclosure also relates to methods of classifying a sample as a pre-frontal cortex and/or cerebellum sample, as well as to oligonucleotide microarrays contg. probes for genes which are differentially expressed in pre-frontal cortex and cerebellum.

L12 ANSWER 35 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:624910 CAPLUS <<LOGINID::20100206>>
DN 140:35164
TI Proteomics in biomarker discovery and drug development
AU He, Qing-Yu; Chiu, Jen-Fu
CS Department of Chemistry, Open Laboratory of Chemical Biology of the Institute of Molecular Technology for Drug Discovery and Synthesis, University of Hong Kong, Hong Kong, Peop. Rep. China
SO Journal of Cellular Biochemistry (2003), 89(5), 868-886 CODEN: JCBDD5; ISSN: 0730-2312
PB Wiley-Liss, Inc.
DT Journal; General Review
LA English
AB A review. Proteomics is a research field aiming to characterize mol. and cellular dynamics in protein expression and function on a global level. The introduction of proteomics has been greatly broadening our view and accelerating our path in various medical researches. The most significant advantage of

proteomics is its ability to examine a whole proteome or sub-proteome in a single expt. so that the protein alterations corresponding to a pathol. or biochem. condition at a given time can be considered in an integrated way. Proteomic technol. has been extensively used to tackle a wide variety of medical subjects including biomarker discovery and drug development. By complement with other new technique advances in genomics and bioinformatics, proteomics has a great potential to make considerable contribution to biomarker identification and to revolutionize drug development process. This article provides a brief overview of the proteomic technologies and their application in biomarker discovery and drug development.
OSC.G 55 THERE ARE 55 CAPLUS RECORDS THAT CITE THIS RECORD (55 CITINGS)
RE.CNT 212 THERE ARE 212 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 36 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:621902 CAPLUS <<LOGINID::20100206>>
DN 139:227736
TI Microarray analysis of peroxisome proliferator-activated receptor-.gamma. induced changes in gene expression in macrophages
AU Hodgkinson, Conrad P.; Ye, Shu
CS Human Genetics Division, University of Southampton School of Medicine, Southampton, UK
SO Biochemical and Biophysical Research Communications (2003), 308(3), 505-510 CODEN: BBRCA9; ISSN: 0006-291X
PB Elsevier Science
DT Journal
LA English
AB We used a combination of expression microarray and Northern blot analyses to identify target genes for peroxisome proliferator-activated receptor (PPAR) .gamma. in RAW264.7 macrophages. PPAR.gamma. natural ligand 15-deoxy-.DELTA.12,14 prostaglandin and synthetic ligands ciglitazone and rosiglitazone increased the expression of scavenger receptor CD36 and ATP-binding cassette transporter A1, as well as adipophilin (a lipid droplet coating protein involved in intracellular lipid storage and transport), calpain (a protease implicated in ABCA1 protein degrdn.), and ADAM8 (a disintegrin and metalloprotease protein involved in cell adhesion). These findings are relevant to understanding the effect of PPAR.gamma. activation on gene expression and cognate pathways in macrophages.
OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 37 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:615849 CAPLUS <<LOGINID::20100206>>
DN 139:174864
TI Identification of cartilage disease markers by gene expression profile analysis and use in drug screening
IN Aoki, Mikio; Harada, Hideyuki
PA Sumitomo Pharmaceuticals Co., Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 64 pp. CODEN: JKXXAF
DT Patent
LA Japanese

FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI JP 2003225093 A 20030812 JP 2002-348073 20021129
PRAI JP 2001-367993 A 20011130
AB Nucleotide and protein sequences of cartilage disease markers, probes and primers targeting those sequences, antibodies to those proteins, and their use in screening of compds. modulating the expression of those genes as candidate for therapeutic agents for cartilage diseases, are disclosed. Expression profile anal. in osteoarthritis rat model and human patients identified acetyl-CoA acetyltransferase 1, Rev-ErbA, selenoprotein P, aquaporin 1, BMP-3b, FK506-binding protein 1A, apolipoprotein E, acyl-CoA synthetase 5, epoxide hydrolase 1, glutamine synthase as markers for cartilage diseases. FK506-binding protein 1A inhibitor FK506, aquaporin 1 inhibitor Phloretin, epoxide hydrolase 1 inhibitors valproic acid and GdCl3.6H2O, glutamine synthase inhibitor L-methionine sulfoximine were found to facilitate cartilage differentiation. L-methionine sulfoximine, FK506, and Phloretin also showed suppressive effect on joint cartilage diseases. Phloretin also inhibited PGE2 prodn. induced by IL-1.beta. stimulation, indicating suppression of inflammation in osteoarthritis.

L12 ANSWER 38 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:584325 CAPLUS <<LOGINID::20100206>>
DN 139:361886
TI Acute induction of conserved synaptic signaling pathways in Drosophila melanogaster
AU Hoeffer, C. A.; Sanyal, S.; Ramaswami, M.
CS Department of Molecular and Cellular Biology, University of Arizona, Tucson, AZ, 85721, USA
SO Journal of Neuroscience (2003), 23(15), 6362-6372 CODEN: JNRSDS; ISSN: 0270-6474
PB Society for Neuroscience
DT Journal
LA English
AB Analyses of early mol. and cellular events assocd. with long-term plasticity remain hampered in Drosophila by the lack of an acute procedure to ***activate*** signal transduction pathways, gene ***expression*** ***patterns*** , and other early cellular events assocd. with long-term synaptic ***change*** . Here the authors describe the development and first use of such a technique. Bursts of neural activity induced in Drosophila comatosets and CaP60AKumts mutants, with conditional defects in N-ethylmaleimide-sensitive fusion factor 1 and sarco-endoplasmic reticulum Ca2+ ATPase, resp., result in persistent (> 4 h) activation of neuronal extracellular signal-regulated kinase (ERK). ERK activation at the larval neuromuscular junction coincides with rapid redn. of synaptic Fascidin II; in soma, nuclear translocation of activated ERK occurs together with increased transcription of the immediate-early genes Fos and c/EBP (CCAAT element binding protein). The effect of "seizure-stimulation" on ERK activation requires neural activity and is mediated through activation of MEK (MAPK/erk kinase), the MAPK (mitogen-activated protein kinase kinase) that functions upstream of ERK. The authors' results provide direct proof for the conservation of synaptic signaling pathways in arthropods, demonstrate the utility of a new genetic tool for anal. of synaptic plasticity in Drosophila, and potentially enable new proteomic and genomic analyses of activity-regulated mols. in an important model organism.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)

RE.CNT 90 THERE ARE 90 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 39 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:568458 CAPLUS <<LOGINID::20100206>>
DN 139:243624
TI Identification of genes differentially expressed in mouse mammary epithelium transformed by an activated .beta.-catenin
AU Renou, Jean-Pierre; Bierie, Brian; Miyoshi, Keiko; Cui, Yongzhi; Djiane, Jean; Reichenstein, Moshe; Shani, Moshe; Hennighausen, Lothar
CS National Institute of Diabetes and Digestive and Kidney Diseases, 1Laboratory of Genetics and Physiology, National Institutes of Health, Bethesda, MD, 20892, USA
SO Oncogene (2003), 22(29), 4594-4610 CODEN: ONCNES; ISSN: 0950-9232
PB Nature Publishing Group
DT Journal
LA English
AB .beta.-Catenin is an executor of Wnt signaling and it can control cell fate and specification. Deletion of exon 3 from the endogenous .beta.-catenin gene in differentiating mammary alveolar epithelium of the mouse results in the generation of an activated protein that lacks amino acids 5-80. This is accompanied by a loss of mammary epithelial differentiation and a transdifferentiation process to squamous metaplasias. To further understand the mol. process of transdifferentiation, the expression of genes in mammary tissue was profiled in the absence and presence of activated of .beta.-catenin. Microarrays were generated that carry about 8500 cDNA clones with approx. 6000 obtained from mammary tissue. Mutant tissues, which had undergone either partial (TD1) or complete (TD2) squamous transdifferentiation, were compared with wild-type mammary tissue. Four groups of genes were identified. Group 1 contained genes whose expression was induced in both mutant tissues. Groups 2 and 3 contained genes that were active preferentially in TD2 and TD1, resp. Group 4 contained genes suppressed in both samples. Using this approach, known and unknown genes activated in the transdifferentiation process were identified. A new 20 kDa protein (PANE1) induced upon transdifferentiation was nuclear in nonconfluent cells and cytoplasmic in confluent or dividing cells. Lastly, stabilization of .beta.-catenin resulted in the retention of differentiated epithelium upon involution and altered activities of several proteases in transdifferentiated mammary epithelium.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 40 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:563751 CAPLUS <<LOGINID::20100206>>
DN 139:257082
TI Purification of a polyphenol oxidase isoform from potato (Solanum tuberosum) tubers
AU Marri, Costanza; Frazzoli, Alessandra; Hochkoeppler, Alejandro; Poggi, Valeria
CS Department of Industrial Chemistry, University of Bologna, Bologna, I-40136, Italy
SO Phytochemistry (Elsevier) (2003), 63(7), 745-752 CODEN: PYTCAS; ISSN: 0031-9422
PB Elsevier Science B.V.
DT Journal
LA English
AB A different expression pattern of polyphenol oxidases has been obsd. during storage in cultivars of potato (Solanum tuberosum L.) featuring different length of dormancy: a short-dormant cultivar showed, at the end of the dormancy, both the highest polyphenol oxidase activity and the largest no. of enzyme isoforms. An isoform of polyphenol oxidase isolated at the end of the physiol. dormancy from a short-dormant cultivar has been purified to homogeneity by means of column chromatog. on Ph Sepharose and on Superdex 200. The purifn. factor has been detd. equal to 88, and the mol. mass of the purified isoform has been estd. to be 69 and 340 kDa by SDS-PAGE and gel filtration on Superdex 200, resp., indicating this PPO isoform as a multimer. The corresponding zymogram features a diffused single band at the cathodic region of the gel and the pI of this polyphenol oxidase has been calcd. equal to 6.5.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 41 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:560035 CAPLUS <<LOGINID::20100206>>
DN 139:80225
TI Protein and cDNA sequences of 9.35-kilodalton human endothelial differentiation factor 1-like protein and their therapeutic uses
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 32 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI CN 1363571 A 20020814 CN 2001-105043 20010105
PRAI CN 2001-105043 20010105
AB The invention provides protein and cDNA sequences of a novel 9.35-kilodalton human protein, designated as "endothelial differentiation factor 1-9.35", which has similar expression pattern to that of known endothelial differentiation factor 1. The invention relates to expression of endothelial differentiation factor 1-like protein in E. coli BL21(DE3)plySs transfected with plasmid pET-28(+). The invention also relates to prepn. of antibody against endothelial differentiation factor 1-like protein. The invention further relates to the uses of the endothelial differentiation factor 1-like protein in treatment of endothelial differentiation factor 1-related diseases (such as neoplasm, blood disease, HIV infection, immune disease, inflammation, etc).

L12 ANSWER 42 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:553614 CAPLUS <<LOGINID::20100206>>
DN 139:304603
TI AtNRAMP3, a multispecific vacuolar metal transporter involved in plant responses to iron deficiency
AU Thomine, Sebastien; Lelievre, Francoise; Debarbieux, Elise; Schroeder, Julian I.; Barbier-Brygoo, Helene
CS Institut des Sciences du Vegetal, UPR2355, CNRS, Gif-sur-Yvette, 91198, Fr.

SO Plant Journal (2003), 34(5), 685-695 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Publishing Ltd.
DT Journal
LA English
AB Metal homeostasis is crit. for the survival of living organisms, and metal transporters play central roles in maintaining metal homeostasis in the living cells. The authors have investigated the function of a metal transporter of the NRAMP family, AtNRAMP3, in Arabidopsis thaliana. A previous study showed that AtNRAMP3 expression is upregulated by iron (Fe) starvation and that AtNRAMP3 protein can transport Fe. In the present study, the authors used AtNRAMP3 promoter .beta.-glucuronidase (GUS) fusions to show that AtNRAMP3 is expressed in the vascular bundles of roots, stems, and leaves under Fe-sufficient conditions. This suggests a function in long-distance metal transport within the plant. Under Fe-starvation conditions, the GUS ***activity*** driven by the AtNRAMP3 promoter is upregulated without any ***change*** in the ***expression*** ***pattern***. The authors analyze the impact of AtNRAMP3 disruption and overexpression on metal accumulation in plants. Under Fe-sufficient conditions, AtNRAMP3 overexpression or disruption does not lead to any change in the plant metal content. Upon Fe starvation, AtNRAMP3 disruption leads to increased accumulation of manganese (Mn) and zinc (Zn) in the roots, whereas AtNRAMP3 overexpression downregulates Mn accumulation. In addn., overexpression of AtNRAMP3 downregulates the expression of the primary Fe uptake transporter IRT1 and of the root ferric chelate reductase FRC2. Expression of AtNRAMP3::GFP fusion protein in onion cells or Arabidopsis protoplasts shows that AtNRAMP3 protein localizes to the vacuolar membrane. The authors propose that AtNRAMP3 influences metal accumulation and IRT1 and FRC2 gene expression by mobilizing vacuolar metal pools to the cytosol.
OSC.G 106 THERE ARE 106 CAPLUS RECORDS THAT CITE THIS RECORD (106 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 43 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:543964 CAPLUS <<LOGINID::20100206>>
DN 139:115991
TI CEACAM1 is a potent regulator of B cell receptor complex-induced activation
AU Greicius, Gediminas; Severinson, Eva; Beauchemin, Nicole; Oebrink, Bjoern; Singer, Bernhard B.
CS Department of Cell and Molecular Biology, Medical Nobel Institute, Karolinska Institutet, Stockholm, Swed.
SO Journal of Leukocyte Biology (2003), 74(1), 126-134 CODEN: JLBIE7; ISSN: 0741-5400
PB Federation of American Societies for Experimental Biology
DT Journal
LA English
AB Carcinoembryonic antigen-related cell adhesion mol. 1 (CEACAM1, CD66a) is a member of the Ig superfamily, previously characterized as an adhesion and signaling mol. in epithelial, endothelial, and hematopoietic cells. Here, we show that the CEACAM1 isoform ***expression*** ***pattern*** is ***different*** in nonactivated and ***activated*** primary mouse B lymphocytes and that CEACAM1 influences B cell receptor complex-mediated activation. A CEACAM1-specific monoclonal antibody strongly triggered proliferation of mouse B cells when combined with surface IgM crosslinking. However, anti-CEACAM1 was not mitogenic when added alone. The proliferation was more pronounced and lasted longer as compared with other activators of B cells, such as anti-IgM in the presence of interleukin-4 or lipopolysaccharide. A similar, costimulatory effect was exerted by CEACAM1-expressing fibroblasts, indicating that homophilic CEACAM1-CEACAM1 cell-mediated binding is the physiol. stimulus for CEACAM1-triggered B cell signaling. The anti-CEACAM1/anti-IgM-activated cells aggregated in a lymphocyte function-assocd. antigen-1-dependent manner. Furthermore, cells that were activated by anti-CEACAM1/anti-IgM secreted Ig but did not go through Ig class-switching. Anti-CEACAM1 induced phosphorylation of c-Jun N-terminal kinase (stress-activated protein kinase) but did not activate the extracellular signal-regulated kinase or p38 mitogen-activated protein kinases.
OSC.G 25 THERE ARE 25 CAPLUS RECORDS THAT CITE THIS RECORD (25 CITINGS)
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 44 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:537976 CAPLUS <<LOGINID::20100206>>
DN 139:81614
TI Immortalized human keratinocyte cell lines with different telomerase activity for drug screening and cancer genetics
IN Iizuka, Kazuko; Nakanishi, Hiroshi; Hanaoka, Fumio; Chiba, Katsuyoshi
PA Yakult Honsha Co., Ltd., Japan; Institute of Physical and Chemical Research
SO Jpn. Kokai Tokkyo Koho, 10 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI JP 2003199561 A 20030715 JP 2001-401139 20011228
PRAI JP 2001-401139 20011228
AB A transformed immortalized cell line derived from normal human cells having telomerase activity and life prolongation cell line having inactivated telomerase activity from the same tissue of the same organism, for use in screening cancer-assocd. genes and anticancer agents, are disclosed. The life prolongation cell line has Rb protein function inactivated. Those cell lines are derived from cells in which multiplying and cell division phases are easily distinguished. Gene expression profiles in those two cell lines are analyzed to identify genes assocd. with cancer. The immortalized and life prolongation cell lines were derived from human keratinocyte. Anal. of gene expression profile in those cell lines revealed that relative expression level of topoisomerase II.alpha. binding protein (TII.alpha.BP) and topoisomerase 2.alpha. were altered. Some plant exts. showed activities for inhibiting hyaluronic acid degrdn.

L12 ANSWER 45 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:537779 CAPLUS <<LOGINID::20100206>>
DN 139:212737
TI Molecular heterogeneity in acute renal allograft rejection identified by DNA microarray profiling
AU Sarwal, Minnie; Chua, Mei-Sze; Kambham, Neeraja; Hsieh, Szu-Chuan; Satterwhite, Thomas; Masek, Marilyn; Salvatierra, Oscar, Jr.
CS Department of Pediatrics, Stanford University, Stanford, CA, USA

SO New England Journal of Medicine (2003), 349(2), 125-138
CODEN: NEJMAG; ISSN: 0028-4793
PB Massachusetts Medical Society
DT Journal
LA English
AB Background: The causes and clin. course of acute rejection vary, and it is not possible to predict graft outcome reliably on the basis of available clin., pathol., and genetic markers. We hypothesized that previously unrecognized mol. heterogeneity might underlie some of the variability in the clin. course of acute renal allograft rejection and in its response to treatment. Methods: We used DNA microarrays in a systematic study of gene-expression patterns in biopsy samples from normal and dysfunctional renal allografts. A combination of exploratory and supervised bioinformatic methods was used to analyze these profiles. Results: We found consistent ***differences*** among the gene- ***expression*** ***patterns*** assocd. with acute rejection, nephrotoxic effects of ***drugs*** , chronic allograft nephropathy, and normal kidneys. The gene-expression patterns assocd. with acute rejection suggested at least three possible distinct subtypes of acute rejection that, although indistinguishable by light microscopy, were marked by differences in immune activation and cellular proliferation. Since the gene-expression patterns pointed to substantial variation in the compn. of immune infiltrates, we used immunohistochem. staining to define these subtypes further. This anal. revealed a striking assocn. between dense CD20+ B-cell infiltrates and both clin. glucocorticoid resistance (P= 0.01) and graft loss (P< 0.001). Conclusions: Systematic anal. of gene-expression patterns provides a window on the biol. and pathogenesis of renal allograft rejection. Biopsy samples from patients with acute rejection that are indistinguishable on conventional histol. anal. reveal extensive differences in gene expression, which are assocd. with differences in immunol. and cellular features and clin. course. The presence of dense clusters of B cells in a biopsy sample was strongly assocd. with severe graft rejection, suggesting a pivotal role of infiltrating B cells in acute rejection.
OSC.G 150 THERE ARE 150 CAPLUS RECORDS THAT CITE THIS RECORD (150 CITINGS)
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 46 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:536894 CAPLUS << LOGINID::20100206>>
DN 139:242113
TI Purification, Kinetic Characterization, and Molecular Cloning of a Novel Enzyme Ecdysteroid-phosphate Phosphatase
AU Yamada, Ryouichi; Sonobe, Haruyuki
CS Faculty of Science and Engineering, Graduate School of Natural Sciences, Department of Life and Functional Material Science, Konan University, Kobe, 658-8501, Japan
SO Journal of Biological Chemistry (2003), 278(29), 26365-26373 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB From eggs of the silkworm Bombyx mori, we isolated a novel enzyme that is involved in the conversion of physiol. inactive conjugated ecdysteroids, such as ecdysone 22-phosphate and 20-hydroxyecdysone 22-phosphate, to active free ecdysteroids. This enzyme, called ecdysteroid-phosphate phosphatase (EPPase), was located in the cytosol fraction and differed from nonspecific lysosomal acid phosphatases in various enzymic properties. EPPase was purified about 3,000-fold to homogeneity by seven steps of column chromatog. The cDNA clone encoding EPPase was isolated by reverse transcription polymerase chain reaction using degenerate primers on the basis of the partial amino acid sequence obtained from purified EPPase and by subsequent 3'- and 5'-rapid amplification of cDNA ends. The full-length cDNA of EPPase was found to be composed of 1620 bp with an open reading frame encoding a protein of 331 amino acid residues. A data base search showed that there was no functional protein with the amino acid sequence identical to that of EPPase. Northern blot anal. revealed that EPPase mRNA was expressed predominantly during gastrulation and organogenesis in nondiapause eggs but was not detected in diapause eggs whose development was arrested at the late gastrula stage. In nondiapause eggs, the developmental ***changes*** in the ***expression*** ***pattern*** of EPPase mRNA corresponded closely to ***changes*** in the enzyme ***activity*** and in the amts. of free ecdysteroids in eggs.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 47 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:512233 CAPLUS << LOGINID::20100206>>
DN 139:162865
TI Differential gene expression profiles and identification of the genes relevant to clinicopathologic factors in colorectal cancer selected by cDNA array method in combination with principal component analysis
AU Tsunoda, Takuya; Koh, Yasuhiro; Koizumi, Fumiaki; Tsukiyama, Shoji; Ueda, Hiroshi; Taguchi, Fumiko; Yamaue, Hiroki; Saijo, Nagahiro; Nishio, Kazuto
CS Department of Surgery and Bioengineering Advanced Clinical Research Center, Institute of Medical Science of Tokyo, Tokyo, 108-8639, Japan
SO International Journal of Oncology (2003), 23(1), 49-59
CODEN: IJONES; ISSN: 1019-6439
PB International Journal of Oncology
DT Journal
LA English
AB The clin. outcome of patients with colorectal cancer frequently varies even if they are at the same clinicopathol. stage. Alternative superior tumor markers of colorectal cancer are needed for prediction of clin. outcome. To clarify the regulatory factors in colorectal cancers, we examd. differential expression profiles using cDNA microarray technique with surgically resected specimens obtained from the patients with colorectal cancer. The gene profiles by an av.-linkage hierarchical clustering anal. were found to be almost separable into two groups: tumor group and normal mucosa group. The relationship between several clinicopathol. factors and cancer related genes were investigated by using statistical analyses including principal component anal. (PCA). C-myc-binding protein MM-1, and c-jun proto-oncogene were identified as possible markers of tumor histol. and clin. prognosis and early growth response protein 1 (EGR1) was selected to play an important role in progression of clin. stage. We conclude that, with PCA method, we successfully selected the genes relevant to clinicopathol. factors using limited population of clin. samples.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 48 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:495562 CAPLUS <<LOGINID::20100206>>
DN 139:196093
TI Differential gene expression in CD8+ cells exhibiting noncytotoxic anti-HIV activity
AU Diaz, Leyla S.; Stone, Mars R.; Mackewicz, Carl E.; Levy, Jay A.
CS Division of Hematology/Oncology, Department of Medicine, University of California, San Francisco, CA, 94143-1270, USA
SO Virology (2003), 311(2), 400-409 CODEN: VIRLAX; ISSN: 0042-6822
PB Elsevier Science
DT Journal
LA English
AB Suppressive subtractive hybridization with polymerase chain reaction was used to identify the gene(s) assocd. with the CD8+ cell noncytotoxic anti-HIV response. The differences in gene expression profiles of CD8+ cells from a pair of discordant HIV-pos. identical twins were studied. Forty-nine genes were identified as expressed at higher levels in the CD8+ cells from the infected twin that inhibited viral replication. The differential expression of these genes was then evaluated using Q-PCR to det. if this gene expression pattern is evident in CD8+ cells from other HIV-pos. subjects showing this antiviral activity. Three genes, including one unknown, were found to have significantly increased expression in antiviral CD8+ cells.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 49 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:494443 CAPLUS <<LOGINID::20100206>>
DN 139:243566
TI Gene expression profiles in different stages of mouse spermatogenic cells during spermatogenesis
AU Yu, Zuoren; Guo, Rui; Ge, Yehua; Ma, Jing; Guan, Jikui; Li, Sai; Sun, Xiaodong; Xue, Shepu; Han, Daishu
CS Department of Cell Biology, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, 100005, Peop. Rep. China
SO Biology of Reproduction (2003), 69(1), 37-47 CODEN: BIREBV; ISSN: 0006-3363
PB Society for the Study of Reproduction
DT Journal
LA English
AB During spermatogenesis, diploid stem cells differentiate, undergo meiosis and spermiogenesis, and transform into haploid spermatozoa. Various factors have been demonstrated to regulate this marvelous process of differentiation, but the expression of only a few genes specifically involved in spermatogenesis has been studied. In the present study, different types of spermatogenic cells were isolated from Balb/c mice testes of different ages using the velocity sedimentation method, and we detd. the expression profiles of 1176 known mouse genes in six different types of mouse spermatogenic cells (primitive type A spermatogonia, type B spermatogonia, preleptotene spermatocytes, pachytene spermatocytes, round spermatids, and elongating spermatids) using Atlas cDNA arrays. Of the 1176 genes on the Atlas Mouse 1.2 cDNA Expression Arrays, we detected 181 genes in primitive type A spermatogonia, 256 in type B spermatogonia, 221 in preleptotene spermatocytes, 160 in pachytene spermatocytes, 141 in round spermatids, and 126 in elongating spermatids. A no. of genes were detected as differential expression (up-regulation or down-regulation). Fourteen of the differentially expressed genes have been further confirmed by reverse transcription-polymerase chain reaction for their expression characterizations in different types of spermatogenic cells. These results provide more information for further studies into spermatogenesis-related genes and may lead to the identification of genes with potential relevance to spermatogenesis.
OSC.G 38 THERE ARE 38 CAPLUS RECORDS THAT CITE THIS RECORD (38 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 50 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:492536 CAPLUS <<LOGINID::20100206>>
DN 139:48269
TI Genes differentially regulated during MYCN activation in neuroblastoma cells
IN Stuart, Susan G.; Nuchtern, Jed G.; Plon, Sharon E.; Shohet, Jason M.
PA USA
SO U.S. Pat. Appl. Publ., 27 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 20030119009 A1 20030626 US 2002-84817 20020225
PRAI US 2001-270784P P 20010223
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The present invention relates to a combination comprising a plurality of cDNAs which are differentially expressed by MYCN activation and which may be used in their entirety or in part to diagnose, to stage, to treat, or to monitor the treatment of a subject with neuroblastoma. The cDNAs represent known and novel genes differentially expressed between a tumor explant from an INSS stage 4 neuroblastoma patient showing amplified MYCN (P4) and a tumor explant from an INSS stage 4 neuroblastoma patient showing non-amplified MYCN (P67). The combination may be used in its entirety or in part, as subsets of 280 down-regulated cDNAs, or of 85 up-regulated cDNAs. Since the cDNAs were identified solely by their differential expression, it is not essential to know a priori the name, structure, or function of the gene or its encoded protein. The usefulness of the cDNAs exists in their immediate value as diagnostics for disorders assocd. with MYCN activation such as neuroblastoma.

L12 ANSWER 51 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:486076 CAPLUS <<LOGINID::20100206>>
DN 139:258861
TI Gene expression profiling - a new approach in the study of myocardial ischemia
AU Simkhovich, Boris Z.; Kloner, Robert A.; Poizat, Coralie; Marjoram, Paul; Kedes, Laurence H.
CS Heart Institute, Good Samaritan Hospital, USA
SO Cardiovascular Pathology (2003), 12(4), 180-185 CODEN: CATHEB; ISSN: 1054-8807
PB Elsevier Science Inc.
DT Journal; General Review

LA English
AB A review. Current technologies make it possible to study thousands of genes simultaneously in the same biol. sample - an approach termed gene expression profiling. Several techniques, including (i) differential display, (ii) serial anal. of gene expression (SAGE), (iii) subtractive hybridization and (iv) gene microarrays (Gene Chips), have been developed. Recently, gene profiling was applied in studying the mechanisms of ischemic injury and ischemic preconditioning. In the case of reversible ischemia caused by one or several brief transient episodes of complete coronary occlusion (as with ischemic preconditioning), or with a more prolonged but partial coronary ligation, many up-regulated genes were related to the "cell survival program". Protective genes included mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK 3), heat shock proteins 70, 27, 22, B-cryst., vascular endothelial growth factor, inducible nitric oxide synthase and plasminogen activator inhibitors 1 and 2. With permanent coronary occlusion lasting from 24 h to several weeks, and resulting in a true myocardial infarction (MI), the list of up-regulated genes included those related to remodeling (e.g., collagens I and III, fibronectin, laminin) and apoptosis (Bax), while many down-regulated genes were related to major energy-generating pathways in the heart, namely, fatty acid metab. Gene ***expression*** ***profiling*** expts. have resulted in the discovery of two ***different*** genetic programs in the heart, namely, a protective program ***activated*** upon brief episodes of transient ischemia and an injury-related one activated in response to irreversible ischemic injury. Searching for factors turning on protective genes, and turning down injury-related ones, is a justifiable approach in developing new therapeutic strategies aimed to fight ischemic heart disease.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 52 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:475363 CAPLUS <<LOGINID::20100206>>
DN 139:112224
TI Positive regulation of gene expression by the catabolite control protein CcpA in Bacillus subtilis
AU Ludwig, Holger; Blencke, Hans-Matti; Schmalisch, Matthias; Detsch, Christian; Merzbacher, Matthias; Stuelke, Joerg
CS Institut fuer Mikrobiologie Biochemie und Genetik, Friedrich-Alexander-Universitaet Erlangen-Nuemberg, Erlangen, D-91058, Germany
SO JMMB Symposium Series (2003), 6(Regulatory Networks in Prokaryotes), 181-186 CODEN: JSSMBE
PB Horizon Scientific Press
DT Journal; General Review
LA English
AB A review. In Bacillus subtilis and other Gram-pos. bacteria, carbon catabolite control is mediated by the pleiotropic regulatory protein CcpA. In addn. to loss of catabolite repression, ccpA mutants exhibit a severe growth defect. This growth defect may result from loss of expression of several genes that are activated by CcpA. Gene ***activation*** by CcpA has been studied at ***different*** levels such as ***proteome*** and transcriptome anal. and by investigation of the regulation of individual genes in wild type and ccpA mutant strains. Important cellular functions such as glycolysis, overflow metab. to excrete excess carbon from the cell, and ammonium assimilation depend on a functional CcpA. While CcpA can act directly as a transcriptional activator to allow expression of ackA and pta genes, its role is indirect for genes of glycolysis. In this case, the accumulation of an intracellular inducer cannot occur in ccpA mutants due to a defect in sugar transport by the phosphoenolpyruvate:sugar phosphotransferase system. Several mutations were isolated that exhibit loss of catabolite repression due to the ccpA mutation but that do not cause a growth defect. These mutations were identified within the ccpA gene or are extragenic suppressors.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 53 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:474317 CAPLUS <<LOGINID::20100206>>
DN 139:286127
TI Identification of hepatic transcriptional changes in insulin-resistant rats treated with peroxisome proliferator activated receptor-.alpha. agonists
AU Frederiksen, K. S.; Wulf, E. M.; Wassermann, K.; Sauerberg, P.; Reckner, J.
CS Department of Molecular Genetics, Novo Nordisk A/S, Bagsvaerd, DK-2880, Den.
SO Journal of Molecular Endocrinology (2003), 30(3), 317-329 CODEN: JMLEEI; ISSN: 0952-5041
PB Society for Endocrinology
DT Journal
LA English
AB Peroxisome proliferator activated receptor (PPAR)-.alpha. controls the expression of multiple genes involved in lipid metab., and activators of PPAR-.alpha., such as fibrates, are commonly used drugs in the treatment of hypertriglyceridemia and other dyslipidemic states. Recent data have also suggested a role for PPAR-.alpha. in insulin resistance and glucose homeostasis. In the present study, we have assessed the transcriptional and physiol. responses to PPAR-.alpha. activation in a diet-induced rat model of insulin resistance. The two PPAR-.alpha. activators, fenofibrate and Wy-14643, were dosed at different concns. in high-fat fed Sprague-Dawley rats, and the transcriptional responses were examd. in liver using cDNA microarrays. In these analyses, 98 genes were identified as being regulated by both compds. From this pool of genes, 27 correlated to the obsd. effect on plasma insulin, including PPAR-.alpha. itself and the leukocyte antigen-related protein tyrosine phosphatase (PTP-LAR). PTP-LAR was downregulated by both compds., and showed upregulation as a result of the high-fat feeding. This regulation was also obsd. at the protein level. Furthermore, downregulation of PTP-LAR by fenofibric acid was demonstrated in rat FaO hepatoma cells in vitro, indicating that the obsd. regulation of PTP-LAR by fenofibrate and Wy-14643 in vivo is mediated as a direct effect of the PPAR agonists on the hepatocytes. PTP-LAR is one of the first genes involved in insulin receptor signaling to be shown to be regulated by PPAR-.alpha. agonists. These data suggest that factors apart from skeletal muscle lipid supply may influence PPAR-.alpha.-mediated amelioration of insulin resistance.
OSC.G 18 THERE ARE 18 CAPLUS RECORDS THAT CITE THIS RECORD (18 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 54 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:464732 CAPLUS <<LOGINID::20100206>>
Correction of: 2002:736054
DN 139:21028 Correction of: 137:246536
TI Differentially expressed transcripts and proteins in kidney cancer and their therapeutic and diagnostic use
IN Algate, Paul A.; Mannion, Jane; Gaiger, Alexander; Gordon, Brian; Harlocker, Susan L.
PA Corixa Corporation, USA
SO PCT Int. Appl., 252 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ---------- --------
PI WO 2002074237 A2 20020926 WO 2002-US10055 20020319
WO 2002074237 A3 20030327 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002254482 A1 20021003 AU 2002-254482 20020319 US 20030109434 A1 20030612 US 2002-102524 20020319
PRAI US 2001-277245P P 20010319 US 2001-343340P P 20011221 WO 2002-US10055 W 20020319
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The authors disclose subtractive hybridization, microarray, and real-time PCR anal. of transcripts overexpressed in kidney cancer. The disclosed transcripts and encoded polypeptides may be useful for diagnosis, prevention and/or treatment of disease.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L12 ANSWER 55 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:462800 CAPLUS <<LOGINID::20100206>>
DN 140:265380
TI Entamoeba histolytica: Expression and DNA binding of CCAAT/enhancer-binding proteins are regulated through the cell cycle
AU Marchat, Laurence A.; Pezet-Valdez, Marisol; Lopez-Camarillo, Cesar; Orozco, Esther
CS Programa Institucional de Biomedicina Molecular, Guillermo Massieu Helguera # 239 Fracc. La Escalera, Ticoman, Escuela Nacional de Medicina y Homeopatia del IPN, Mexico city, 07300, Mex.
SO Experimental Parasitology (2003), 103(1/2), 82-87 CODEN: EXPAAA; ISSN: 0014-4894
PB Elsevier Science
DT Journal
LA English
AB The expression of the C'EBP (CCAAT/enhancer-binding protein)-like protein throughout the cell cycle was evaluated using colchicine-synchronized and serum-starved trophozoites of the phagocytosis-deficient mutant L-6 clone to elucidate the growth regulation in Entamoeba histolytica. The trophozoites of E. histolytica have nuclear and cytoplasmic proteins antigenically related to the human C'EBP.beta.. These proteins exhibit ***differential*** ***expression*** ***pattern*** and DNA-binding ***activity*** during cell cycle progression, indicating that they could be participating in cell cycle regulation. C'EBP-like proteins accumulating in the nucleus during M and G1 phases fail to bind DNA efficiently, suggesting that these proteins require some maturation processes. Increased C'EBP-like protein could be one of the factors that regulate the expression of genes involved in replication and DNA synthesis in E. histolytica.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 56 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:447483 CAPLUS <<LOGINID::20100206>>
DN 139:241182
TI Comparative microarray analysis of gene expression during activation of human peripheral blood T cells and leukemic Jurkat T cells
AU Lin, Zhaosheng; Fillmore, G. Chris; Um, Tae-Hyun; Ekenitoba-Johnson, Kojo S. J.; Lim, Megan S.
CS ARUP Institute for Clinical and Experimental Pathology, University of Utah, Salt Lake City, UT, 84132, USA
SO Laboratory Investigation (2003), 83(6), 765-776 CODEN: LAINAW; ISSN: 0023-6837
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB Activation of T cells involves a complex cascade of signal transduction pathways linking T-cell receptor engagement at the cell membrane to the transcription of multiple genes within the nucleus. The T-cell leukemia-derived cell line Jurkat has generally been used as a model system for the activation of T cells. However, genome-wide comprehensive studies investigating the activation status, and thus the appropriateness, of this cell line for this purpose have not been performed. We sought to compare the transcriptional profiles of phenotypically purified human CD2+ T cells with those of Jurkat T cells during T-cell activation, using cDNA microarrays contg. 6912 genes. About 300 genes were up-regulated by more than 2-fold during activation of both peripheral blood (PB) T cells and Jurkat T cells. The no. of down-regulated genes was significantly lower than that of up-regulated genes. Only 79 genes in PB T cells and 37 genes in Jurkat T cells were down-regulated by more than 2-fold during activation. Comparison of gene expression during activation of Jurkat and PB T cells revealed a common set of genes that were up-regulated, such as Rho GTPase-activating protein 1, SKP2, CDC25A, T-cell specific transcription factor 7, cytoskeletal proteins, and signaling mols. Genes that were commonly down-regulated in both PB T cells and Jurkat T cells included CDK inhibitors (p16, p19, p27), proapoptotic caspases, and the transcription factors c-fos and jun-B. After activation, 71 genes in PB T cells and only 3 genes in Jurkat T cells were up-regulated 4-fold or more. Of these up-regulated genes and expressed sequence tags, 44 were constitutively expressed at high levels in nonactivated Jurkat cells. Quant. real-time RT-PCR anal. confirmed our microarray data. Our findings indicate that although there is significant overlap in the activation-assocd. transcriptional profiles in PB T cells compared with Jurkat T cells, there is a subset of genes showing ***differential*** ***expression*** ***patterns*** during the ***activation*** of the two cell types.

OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 57 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:442041 CAPLUS <<LOGINID::20100206>>
DN 139:226226
TI Alternative splicing variants of dual specificity tyrosine phosphorylated and regulated kinase 1B exhibit distinct patterns of expression and functional properties
AU Leder, Susanne; Czajkowska, Hanna; Maenz, Barbara; de Graaf, Katrin; Barthel, Andreas; Joost, Hans-Georg; Becker, Walter
CS Medizinische Fakultaet der RWTH Aachen, Institut fuer Pharmakologie und Toxikologie, Aachen, 52075, Germany
SO Biochemical Journal (2003), 372(3), 881-888 CODEN: BIJOAK; ISSN: 0264-6021
PB Portland Press Ltd.
DT Journal
LA English
AB The dual specificity tyrosine phosphorylated and regulated kinase (DYRK) family of protein kinases is a group of evolutionarily conserved protein kinases that have been characterized as regulators of growth and development in mammals, Drosophila and lower eukaryotes. In the present study, we have characterized three splicing variants of DYRK1B (DYRK1B-p65, DYRK1B-p69 and DYRK1B-p75) with ***different*** ***expression*** ***patterns*** and enzymic ***activities*** . DYRK1B-p65 and DYRK1B-p69 exhibited similar, but not identical, patterns of expression in mouse tissues, with the highest protein levels found in the spleen, lung, brain, bladder, stomach and testis. In contrast, DYRK1B-p75 was detected specifically in skeletal muscles, in the neuronal cell line GT1-7 and also in differentiated, adipocyte-like 3T3-L1 cells, but not in undifferentiated 3T3-L1 preadipocytes. A comparison of the mouse and human Dyrk1b genomic and cDNA sequences defined the alternative splicing events that produce the variants of DYRK1B. In DYRK1B-p75, transcription starts with exon 1B instead of exon 1A, generating a new translation start, which extends the open reading frame by 60 codons. This gene structure suggests that alternative promoters direct the expression of DYRK1B-p69 and DYRK1B-p75. Both splicing variants exhibited kinase activity in vitro and contained phosphotyrosine when expressed in COS-7 cells. Owing to differential recognition of the 3'-splice site in exon 9, DYRK1B-p65 differs from DYRK1B-p69 by the absence of 40 amino acids within the catalytic domain. DYRK1B-p65 lacked kinase activity in vitro and did not contain phosphotyrosine. DYRK1B-p69 and DYRK1B-p75 stimulated reporter gene activity driven by the f or kh ead in r habdosarcoma (FKHR)-dependent glucose-6-phosphatase promoter more strongly when compared with DYRK1B-p65, indicating that the DYRK1B splicing variants exhibit functional differences.
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 58 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:415149 CAPLUS <<LOGINID::20100206>>
DN 139:243467
TI Microarray analysis of somitogenesis reveals novel targets of different WNT signaling pathways in the somitic mesoderm
AU Buttitta, Laura; Tanaka, Tetsuya S.; Chen, Alice E.; Ko, Minoru S. H.; Fan, Chen-Ming
CS Department of Embryology, Carnegie Institution of Washington, Baltimore, MD, 21210, USA
SO Developmental Biology (San Diego, CA, United States) (2003), 258(1), 91-104 CODEN: DEBIAO; ISSN: 0012-1606
PB Elsevier
DT Journal
LA English
AB WNT signaling plays a major role in patterning the dermomyotome of the somitic mesoderm. However, knowledge of downstream target genes and their regulation is limited. To identify new genes involved in the development and early patterning of the somite, we performed a comparison of gene expression by microarray between the presomitic mesoderm and the 5 most recently formed somites of the mouse at embryonic day 9.5. We identified 207 genes upregulated and 120 genes downregulated in somite formation. Expression anal. and functional categorization of these genes demonstrate this to be a diverse pool that provides a valuable resource for studying somite development. Thus far, we have found three genes expressed in the dermomyotome of the early somite. Consistent with their ***expression*** ***patterns*** , these genes are transcriptional targets of WNT signals, but display ***differential*** ***activation*** by different WNTs. We further demonstrate that 1 of these genes, Troy, is a direct target of canonical WNT signaling, while the other 2 genes, Selp and Arl4, are not. Thus, our microarray study using microdissected tissues not only provides global information on gene expression during somite development, it also provides novel targets to study the inductive signaling pathways that direct somite patterning.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 59 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:409464 CAPLUS <<LOGINID::20100206>>
DN 139:144380
TI Evolutionary divergence of platelet-derived growth factor alpha receptor signaling mechanisms
AU Hamilton, T. Guy; Klinghoffer, Richard A.; Corrin, Philip D.; Soriano, Philippe
CS Program in Developmental Biology and Division of Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA, 98109, USA
SO Molecular and Cellular Biology (2003), 23(11), 4013-4025 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB Receptor tyrosine kinases (RTKs) direct diverse cellular and developmental responses by stimulating a relatively small no. of overlapping signaling pathways. Specificity may be detd. by RTK ***expression*** ***patterns*** or by ***differential*** ***activation*** of individual signaling pathways. To address this issue the authors generated knock-in mice in which the extracellular domain of the mouse platelet-derived growth factor alpha receptor (PDGF.alpha.R) is fused to the cytosolic domain of Drosophila Torso (.alpha.Tor) or the mouse fibroblast growth factor receptor 1 (.alpha.FR). .alpha.Tor Homozygous embryos

exhibit significant rescue of neural crest and angiogenesis defects normally found in PDGF.alpha.R-null embryos yet fail to rescue skeletal or extraembryonic defects. This phenotype was assocd. with the ability of .alpha.Tor to stimulate the mitogen-activated protein (MAP) kinase pathway to near wild-type levels but failure to completely activate other pathways, such as phosphatidylinositol (PI) 3-kinase. The .alpha.FR chimeric receptor fails to rescue any aspect of the PDGF.alpha.R-null phenotype. Instead, .alpha.FR expression leads to a gain-of-function phenotype highlighted by ectopic bone development. The .alpha.FR phenotype was assocd. with a failure to limit MAP kinase signaling and to engage significant PI3-kinase response. These results suggest that precise regulation of divergent downstream signaling pathways is crit. for specification of RTK function.
OSC.G 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 60 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:395122 CAPLUS <<LOGINID::20100206>>
DN 139:146044
TI Proteome analysis of secreted proteins during osteoclast differentiation using two different methods: Two-dimensional electrophoresis and isotope-coded affinity tags analysis with two-dimensional chromatography
AU Kubota, Kazuishi; Wakabayashi, Kenji; Matsuoka, Tatsuji
CS Biomedical Research Laboratories, Sankyo, Tokyo, Japan
SO Proteomics (2003), 3(5), 616-626 CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
AB Bone is maintained by two cell types, bone-forming osteoblasts and bone-resorbing osteoclasts. Osteoblasts express two factors, osteoprotegerin and receptor activator of NF-.kappa.B ligand (RANKL), inhibiting and promoting osteoclast differentiation, resp. In contrast, modulators of bone resorption expressed by osteoclasts have not been so well studied enough. In the present study, we demonstrate proteome anal. of secreted proteins during osteoclast differentiation to elucidate the mol. mechanism of bone resorption and bone remodeling. To achieve this objective, we chose RAW264.7 cells with RANKL as a homogeneous osteoclast differentiation model and used two methods, two-dimensional gel electrophoresis (2-DE) and isotopecoded affinity tags (ICAT) anal. with two-dimensional liq. chromatog. We found 23 spots in 2-DE and 19 proteins in ICAT anal. which were expressed differently during osteoclast differentiation. These two methods gave us closely related but different information about proteins, suggesting they are complementary or at least supplementary methods at present. Cathepsins, osteopontin, legumain, macrophage inflammatory protein-1.alpha., and other proteins were obsd. as up- or down-regulated proteins and are discussed in the context of osteoclast differentiation and bone resorption. In addn. to confirming previous observations, this study indicates novel proteins related to osteoclast differentiation which are potential therapeutic targets for the treatment of bone diseases, such as osteoporosis.
OSC.G 41 THERE ARE 41 CAPLUS RECORDS THAT CITE THIS RECORD (41 CITINGS)
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 61 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:382370 CAPLUS <<LOGINID::20100206>>
DN 139:255840
TI Quantitative cDNA-AFLP analysis for genome-wide expression studies
AU Breyne, P.; Dreesen, R.; Cannoot, B.; Rombaut, D.; Vandepoele, K.; Rombauts, S.; Vanderhaeghen, R.; Inze, D.; Zabeau, M.
CS Flanders Interuniversity Institute for Biotechnology, Department of Plant Systems Biology, Ghent University, Ghent, 9000, Belg.
SO Molecular Genetics and Genomics (2003), 269(2), 173-179 CODEN: MGGOAA; ISSN: 1617-4615
PB Springer-Verlag
DT Journal
LA English
AB An improved cDNA-AFLP method for genome-wide expression anal. has been developed. We demonstrate that this method is an efficient tool for quant. transcript profiling and a valid alternative to microarrays. Unique transcript tags, generated from reverse-transcribed mRNA by restriction enzymes, were screened through a series of selective PCR amplifications. Based on in silico anal., an enzyme combination was chosen that ensures that at least 60% of all the mRNAs were represented by an informative sequence tag. The sensitivity and specificity of the method allows one to detect poorly expressed genes and distinguish between homologous sequences. Accurate gene ***expression*** ***profiles*** were detd. by quant. anal. of band intensities, and subtle ***differences*** in transcriptional ***activity*** were revealed. A detailed screen for cell cycle-modulated genes in tobacco demonstrates the usefulness of the technol. for genome-wide expression anal.
OSC.G 76 THERE ARE 76 CAPLUS RECORDS THAT CITE THIS RECORD (76 CITINGS)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 62 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:380381 CAPLUS <<LOGINID::20100206>>
DN 139:99249
TI Different mechanisms of syndecan-1 activation through a fibroblast-growth-factor-inducible response element (FIRE) in mucosal and cutaneous wounds
AU Rautava, J.; Soukka, T.; Heikinheimo, K.; Miettinen, P. J.; Happonen, R.-P.; Jaakkola, P.
CS Department of Oral and Maxillofacial Surgery, Institute of Dentistry, University of Turku, Turku, FIN-20520, Finland
SO Journal of Dental Research (2003), 82(5), 382-387 CODEN: JDREAF; ISSN: 0022-0345
PB International Association for Dental Research
DT Journal
LA English
AB Syndecan-1 expression is enhanced in cutaneous and mucosal wounds. We have previously demonstrated that wounding-induced syndecan-1 expression in the skin occurs transcriptionally, through a fibroblast-growth-factor-inducible element (FIRE). Here, we show that FIRE is also activated in mucosal wounds. However, both the ***expression*** ***patterns*** and the ***activation*** mechanisms of FIRE are ***different*** from those in the skin. In the mucosa in vivo, the activation starts and ends earlier than in cutaneous wounds. FIRE is first detected at around 12 h in

keratinocytes, and the activation declines by the third day after wounding occurs. The activation is seen on the migrating sheet of epithelial mucosa, as in the case of cutaneous wounding. In contrast to the situation in vivo, organ-cultured mucosal wounds exhibit no FIRE activity, while organ-cultured cutaneous wounds show robust activity. Activation in mucosal wounds is enhanced, however, by the application of epidermal growth factor. This suggests that exogenous growth factor activity is required for activation of syndecan-1 in mucosal wounds but not in cutaneous wounds.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 63 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:379514 CAPLUS <<LOGINID::20100206>>
DN 139:98771
TI Proteomic analyses in Waldenstrom's macroglobulinemia and other plasma cell dyscrasias
AU Mitsiades, Constantine S.; Mitsiades, Nicholas; Treon, Steven P.; Anderson, Kenneth C.
CS Jerome Lipper Multiple Myeloma Center, Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, MA, USA
SO Seminars in Oncology (2003), 30(2), 156-160 CODEN: SOLGAV; ISSN: 0093-7754
PB W. B. Saunders Co.
DT Journal; General Review
LA English
AB A review. The proteomic anal. of tumor cells emerges as a key complement to gene expression profiling, primarily because regulation of protein expression (at the translational and post-translational levels) can buffer the magnitude of changes occurring at the gene transcription level, in order to fine tune cellular functions. Herein we describe the concept of proteomic anal. of the signaling state of tumor cells, as well as its application in the study of signaling pathways in plasma cell dyscrasias, such as Waldenstrom's macroglobulinemia (WM) and multiple myeloma (MM). Comparative studies of WM vs. MM cells at baseline and in the setting of drug treatment reveals proteomic profiles of the signaling state with significant overlap (that could reflect a putative B-cell lineage-related ***proteomic*** signature), but also distinct ***differences*** , possibly associd. with ***differential*** features in the biol. behavior and ***drug*** senstivity of these diseases. These proteomic studies pave the way for a more comprehensive insight into the mol. basis of WM vs. other B-cell malignancies.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 64 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:368080 CAPLUS <<LOGINID::20100206>>
DN 139:206872
TI Ca2+-handling proteins and heart failure: Novel molecular targets?
AU Prestle, J.; Quinn, F. R.; Smith, G. L.
CS Dept. of Cardiovascular Research, Boehringer-Ingelheim Pharma KG, Biberach a.d.R., 88397, Germany
SO Current Medicinal Chemistry (2003), 10(11), 967-981 CODEN: CMCHE7; ISSN: 0929-8673
PB Bentham Science Publishers Ltd.
DT Journal; General Review
LA English
AB A review. Calcium (Ca2+) ions are the currency of heart muscle activity. During excitation-contraction coupling Ca2+ is rapidly cycled between the cytosol (where it activates the myofilaments) and the sarcoplasmic reticulum (SR), the Ca2+ store. These fluxes occur by the transient activity of Ca2+-pumps and -channels. In the failing human heart, ***changes*** in ***activity*** and ***expression*** ***profile*** of Ca2+-handling proteins, in particular the SR Ca2+-ATPase (SERCA2a), are thought to cause an overall redn. in the amt. of SR-Ca2+ available for contraction. In the steady state, the Ca2+-content of the SR is essentially a balance between Ca2+-uptake via SERCA2a pump and Ca2+-release via the cardiac SR Ca2+-release channel complex (Ryanodine receptor, RyR2). This review discusses current pharmacol. options available to enhance cardiac SR Ca2+ content and the implications of this approach as an inotropic therapy in heart failure. Two options are considered: (i) activation of the SERCA2a pump to increase SR Ca2+-uptake, and. (ii) redn. of SR Ca2+-leakage through RyR2. RyR2 forms a macromol. complex with a no. of regulatory proteins that either remain permanently bound or that interact in a time- and/or Ca2+-dependent manner. These regulatory proteins can dramatically affect RyR2 function, e.g. over-expression of the accessory protein FK 506-binding protein 12.6 (FKBP12.6) has recently been shown to reduce SR Ca2+-leak. Recent attempts to design pos. inotropes for chronic administrations have focussed on the use of phosphodiesterase III inhibitors (PDE III inhibitors). These compds., which increase intracellular cAMP-levels, have failed in clin. trials. Therefore medical researchers are seeking new drugs that act through alternative pathways. Novel cardiac inotropes targeting SR Ca2+-cycling proteins may have the potential to fill this gap.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 119 THERE ARE 119 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 65 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:363896 CAPLUS <<LOGINID::20100206>>
DN 139:115963
TI U5A2-13, an antigen originally found on mouse NK-like T cells, is an early inducible cell surface antigen during lymphoid activation
AU Kato, Kazunori; Ikarashi, Yoshinori; Sugahara, Toshiaki; Yasumoto, Atsushi; Sancho, David; Yoshida, Mitsuzi; Takaue, Yoichi; Kobayashi, Yoshiro; Sanchez-Madrid, Francisco; Wakasugi, Hiro
CS Pharmacology Division, National Cancer Center Research Institute, Chuo-ku, Tokyo, 104-0045, Japan
SO Cellular Immunology (2003), 221(1), 27-36 CODEN: CLIMB8; ISSN: 0008-8749
PB Elsevier Science
DT Journal
LA English
AB The authors have previously reported a monoclonal antibody (mAb), U5A2-13 mAb, which originally recognizes a phenotypically and functionally similar population of natural killer (NK)-like T cells. In this study, the authors found that U5A2-13 antigen (U5A2-13) was expressed not only on NK-like T cells but

also on T and B cells during activation. In contrast to the low levels of U5A2-13 on freshly harvested T and B cells, the activation of these cells by various stimuli resulted in high levels of expression of U5A2-13 in vitro and in vivo. Similar to CD69, U5A2-13 is also expressed in most mouse lymphoid cell lines but not in nonhematopoietic cells. U5A2-13 on T cells reached maximal expression by 24 h after stimulation and returned to baseline levels after 3 days. However, U5A2-13 ***differed*** from CD69 since its ***expression*** ***profile*** was ***different*** on CD4+- and CD8+- ***activated*** T cells, phorbol ester- ***activated*** EL-4 cells, and activated splenocytes in CD69-deficient mice. In addn., immunopptn. study indicated that U5A2-13 is not identical to CD69. Importantly, the U5A2-13-pos. population of CD4+ T cells exhibited significant levels of cytokine producing activity upon stimulation. Overall, U5A2-13 is an early inducible cell surface antigen that could be involved in lymphocyte activation.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 66 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:346934 CAPLUS <<LOGINID::20100206>>
DN 138:332911
TI Protein and cDNA sequences of 8.8-kilodalton human adipocyte differentiation-related protein-like protein and their therapeutic uses
IN Mao, Yumin; Xie, Yi
PA Fudan Univ., Peop. Rep. China; Bodao Gene Technology Co., Ltd.
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 34 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1355192 A 20020626 CN 2000-127648 20001201
PRAI CN 2000-127648 20001201
AB The invention provides protein and cDNA sequences of a novel 8.8-kilodalton human protein, designated as "adipocyte differentiation-related protein 8.8", which has similar expression pattern to that of known adipocyte differentiation-related protein. The invention relates to expression of adipocyte differentiation-related protein-like protein in E. coli BL21(DE3)plysS transfected with plasmid pET-28(+). The invention also relates to prepn. of antibody against adipocyte differentiation-related protein-like protein. The invention further relates to the uses of the adipocyte differentiation-related protein-like protein in treatment of adipocyte differentiation-related protein-related diseases (such as obesity, Alexander's disease, night blindness, myocardial infarction, abortion, etc).

L12 ANSWER 67 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:340445 CAPLUS <<LOGINID::20100206>>
DN 138:336393
TI Activation of gene expression in human neutrophils by high mobility group box 1 protein
AU Park, Jong Sung; Arcaroli, John; Yum, Ho-Kee; Yang, Huan; Wang, Haichao; Yang, Kuang-Yao; Choe, Kang-Hyeon; Strassheim, Derek; Pitts, Todd M.; Tracey, Kevin J.; Abraham, Edward
CS Division of Pulmonary Sciences and Critical Care Medicine, University of Colorado Health Sciences Center, Denver, CO, 80262, USA
SO American Journal of Physiology (2003), 284(4, Pt. 1), C870-C879 CODEN: AJPHAP; ISSN: 0002-9513
PB American Physiological Society
DT Journal
LA English
AB High mobility group box 1 (HMGB1) protein, a DNA binding protein that stabilizes nucleosomes and facilitates transcription, was recently identified as a late mediator of endotoxin lethality. High serum HMGB1 levels in patients with sepsis are assocd. with increased mortality, and administration of HMGB1 produces acute inflammation in animal models of lung injury and endotoxemia. Neutrophils occupy a crit. role in mediating the development of endotoxemia-assocd. acute lung injury, but previously it was not known whether HMGB1 could influence neutrophil activation. In the present expts., we demonstrate that HMGB1 increases the nuclear translocation of NF-.kappa.B and enhances the expression of proinflammatory cytokines in human neutrophils. These proinflammatory effects of HMGB1 in neutrophils appear to involve the p38 MAPK, phosphatidylinositol 3-kinase/Akt, and ERK1/2 pathways. The mechanisms of HMGB1-inducted neutrophil activation are distinct from endotoxin-induced signals, because HMGB1 leads to a ***different*** profile of gene ***expression*** , ***pattern*** of cytokine expression, and kinetics of p38 ***activation*** compared with LPS. These findings indicate that HMGB1 is an effective stimulus of neutrophil activation that can contribute to development of a proinflammatory phenotype in diseases characterized by excessively high levels of HMGB1.
OSC.G 88 THERE ARE 88 CAPLUS RECORDS THAT CITE THIS RECORD (88 CITINGS)
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 68 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:322061 CAPLUS <<LOGINID::20100206>>
DN 139:316789
TI Gene expression profiling of phenylbutyrate induced differentiation of glioma cells by cDNA array
AU Sun, Li-jun; Huang, Qiang; Lan, Qing; Du, Zi-wei; Hu, Geng-xi; Wang, Ai-dong
CS Department of Neurosurgery, Suzhou University, Suzhou, 215004, Peop. Rep. China
SO Chinese Journal of Cancer Research (2003), 15(1), 38-42
CODEN: CJCRFH; ISSN: 1000-9604
PB Chinese Journal of Cancer Research
DT Journal
LA English
AB Objective: To analyze the changes of gene expression in phenylbutyrate induced differentiation of glioma cells. Methods: The expression levels of 14000 genes in glioma cells before and after inducement with sodium phenylbutyrate for 2 h or 6 days were evaluated by cDNA array technique and proved by multi-dot blotting. Results: expression of 98 genes in glioma cells showed changes after the inducement. Some genes involved in transcription and translation and some oncogenes are down-regulated, while some gene involved in differentiation or apoptosis are up-regulated. 18 Unknown expression sequencing tag (EST) changed too. Conclusion: A gene expression profile assocd. with differentiation of glioma cells was established.

RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 69 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:302114 CAPLUS <<LOGINID::20100206>>
DN 139:79094
TI Protein expression ***changes*** in the sprague dawley rat liver ***proteome*** following administration of peroxisome proliferator ***activated*** receptor .alpha. and .gamma. ligands
AU White, Ian R.; Man, Wai J.; Bryant, Duncan; Bugelski, Peter; Camilleri, Patrick; Cutler, Paul; Hayes, William; Holbrook, Joanna D.; Kramer, Kerstin; Lord, Peter G.; Wood, John
CS Departments of Genomic and Proteomic Sciences, Medicines Research Centre, GlaxoSmithKline Pharmaceuticals, Stevenage, SG1 2NY, UK
SO Proteomics (2003), 3(4), 505-512 CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
AB Peroxisome proliferator activated receptors (PPARs) are members of the nuclear receptor superfamily and are intimately involved in lipid metab. and energy homeostasis. Activation of these receptors in rodents can lead to hepatomegaly and ultimately hepatic carcinogenesis although the mechanisms by which these processes occur are poorly understood. To further our understanding of these processes and to discriminate between different PPAR mediated signaling pathways, a proteomic approach has been undertaken to identify changes in protein expression patterns in Sprague Dawley rat liver following dosing with a PPAR.alpha. agonist (Wyeth 14643), a PPAR.gamma. agonist (Troglitazone) and a compd. with mixed PPAR.alpha./.gamma. agonist activity (SB-219994). Using one-and-two-dimensional electrophoresis of tissue lysates a diverse range of protein abundance changes was obsd. in these tissues. While a no. of these proteins have PPAR response elements (PPREs) in their resp. promoters, another group was detected whose expression has been documented to be sensitive to peroxisome proliferator administration. Most notably within these groups, proteins involved in lipid catabolism displayed increased expression following drug administration. A further subset of proteins, with less obvious biol. implications, also showed altered expression patterns. Where available, sequences upstream of the coding regions of genes not previously known to have PPREs were searched with positional consensus matrixes for the presence of PPREs in an attempt to validate these changes. Using such an approach putative PPAR.gamma. and PPAR.delta. response elements were discovered upstream of the tubulin .beta. coding region. There was limited overlap in obsd. protein abundance changes between the three groups, and where this was the case (cytosolic epoxide hydrolase, peroxisomal bifunctional enzyme, hydroxymethyl glutaryl CoA, synthase, long chain acyl-CoA thioesterase), expression of these proteins had previously been shown to be under the control of PPAR activity.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 70 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:244462 CAPLUS <<LOGINID::20100206>>
DN 138:380164
TI Identification of genes responsible for osteoblast differentiation from human mesodermal progenitor cells
AU Qi, Huilin; Aguiar, Dean J.; Williams, Shelly M.; La Pean, Alison; Pan, Wei; Verfaillie, Catherine M.
CS Stem Cell Institute, Division of Hematology, Oncology, and Transplantation, Department of Medicine, University of Minnesota Medical School, Minneapolis, MN, 55445, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(6), 3305-3310 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Single human bone marrow-derived mesodermal progenitor cells (MPCs) differentiate into osteoblasts, chondrocytes, adipocytes, myocyts, and endothelial cells. To identify genes involved in the commitment of MPCs to osteoblasts the authors examd. the expressed gene profile of undifferentiated MPCs and MPCs induced to the osteoblast lineage for 1-7 days by cDNA microarray anal. As expected, growth factor, hormone, and signaling pathway genes known to be involved in osteogenesis were activated during differentiation. In addn., 41 transcription factors (TFs) were differentially expressed over time, including TFs with known roles in osteoblast differentiation and TFs not known to be involved in osteoblast differentiation. As the latter group of TFs coclustered with osteogenesis-specific TFs, they may play a role in osteoblast differentiation. When the authors compared the gene ***expression*** ***profile*** of MPCs induced to differentiate to chondroblasts and osteoblasts, significant ***differences*** in the nature and/or timing of gene ***activation*** were seen. These studies indicate that in vitro differentiation cultures in which MPCs are induced to one of multiple cell fates should be very useful for defining signals important for lineage-specific differentiation.
OSC.G 75 THERE ARE 75 CAPLUS RECORDS THAT CITE THIS RECORD (75 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 71 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:244401 CAPLUS <<LOGINID::20100206>>
DN 139:49695
TI ***Drug*** induced ***proteome*** ***changes*** in Candida albicans: Comparison of the effect of .beta.(1,3) glucan synthase inhibitors and two triazoles, fluconazole and itraconazole
AU Bruneau, Jean-Michel; Maillet, Isabelle; Tagat, Eric; Legrand, Raymond; Supatto, Francoise; Fudali, Claude; Le Caer, Jean-Pierre; Labas, Valerie; Lecaque, Dominique; Hodgson, John
CS Infectious Disease Group, Aventis Pharma, Romainville, 93235, Fr.
SO Proteomics (2003), 3(3), 325-336 CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
AB The dimorphic fungus C. albicans is an opportunistic human pathogen. Candidiasis is usually treated with azole antifungal agents. However clin. treatments may fail due to the appearance of resistance to this class of antifungal agents in Candida. Echinocandin derivs. are an alternative for the treatment of these fungal infections and are active against azole resistant isolates of C. albicans. Azoles inhibit the lanosterol 14.alpha.-demethylase,

which is a key enzyme in the synthesis of ergosterol. In contrast, the echinocandin class of antibiotics inhibit noncompetitively .beta.-(1,3)-D-glucan synthesis in vitro. We have investigated the impact of mulundocandin on the proteome of C. albicans and compared it to those of a mulundocandin deriv., as well as to 2 azoles of different structure, fluconazole and itraconazole. The changes in gene expression underlying the antifungal responses were analyzed by comparative 2-D PAGE. Dose dependant responses were kinetically studied on C. albicans grown at 25 degree. (yeast form) in synthetic dextrose medium. This study shows that antifungals with a common mechanism of action lead to comparable effects at the proteome level and that a proteomics approach can be used to distinguish different antifungals, with the promise to become a useful tool to study drugs of unknown mechanism of action.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 72 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:236249 CAPLUS <<LOGINID::20100206>>
DN 139:192338
TI Disparity between changes in mRNA abundance and enzyme activity in Corynebacterium glutamicum:implications for DNA microarray analysis
AU Glanemann, C.; Loos, A.; Gorret, N.; Willis, L. B.; O'Brien, X. M.; Lessard, P. A.; Sinskey, A. J.
CS Department of Biology, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA
SO Applied Microbiology and Biotechnology (2003), 61(1), 61-68 CODEN: AMBIDG; ISSN: 0175-7598
PB Springer-Verlag
DT Journal
LA English
AB The relationship between changes in mRNA abundance and enzyme activity was detd. for three genes over a span of nearly 3 h during amino acid prodn. in Corynebacterium glutamicum. Gene expression changes during C. glutamicum fermns. were examd. by complementary DNA (cDNA) microarrays and by a second method for quantitating RNA levels, competitive reverse transcriptase-PCR (RT-PCR). The results obtained independently by both methods were compared and found to be in agreement, thus validating the quant. potential of DNA microarrays for gene expression profiling. Evidence of a disparity between mRNA abundance and enzyme activity is presented and supports the authors' belief that it is difficult to generally predict protein activity from quant. transcriptome data. Homoserine dehydrogenase, threonine dehydratase, and homoserine kinase are enzymes involved in the biosynthesis of L-isoleucine and other aspartate-derived amino acids in C. glutamicum. The data suggest that different underlying regulatory mechanisms may be connected with the expression of the genes encoding each of these three enzymes. Indeed, whereas in one case the increases in enzyme activity exceeded those in the corresponding mRNA abundance, in another case large increases in the levels of gene expression were not congruent with changes in enzyme activity.
OSC.G 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 73 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:234391 CAPLUS <<LOGINID::20100206>>
DN 138:365536
TI Putative subunits of the maize origin of replication recognition complex ZmORC1-ZmORC5
AU Witmer, Xiaohong; Alvarez-Venegas, Raul; San-Miguel, Phillip; Danilevskaya, Olga; Avramova, Zoya
CS Department of Biological Sciences, Purdue University, West Lafayette, IN, 47907, USA
SO Nucleic Acids Research (2003), 31(2), 619-628 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The finding in animal species of complexes homologous to the products of six Saccharomyces cerevisiae genes, origin of replication recognition complex (ORC), has suggested that ORC-related mechanisms have been conserved in all eukaryotes. In plants, however, the only cloned putative homologs of ORC subunits are the Arabidopsis ORC2 and the rice ORC1. Homologs of other subunits of plant origin have not been cloned and characterized. A striking observation was the absence from the Arabidopsis genome of an obvious candidate gene-homolog of ORC4. This fact raised compelling questions of whether plants, in general, and Arabidopsis, in particular, may have lost the ORC4 gene, whether ORC-homologous subunits function within a complex in plants, whether an ORC complex may form and function without an ORC4 subunit, whether a functional (but not sequence) protein homolog may have taken up the role of ORC4 in Arabidopsis, and whether lack of ORC4 is a plant feature, in general. Here, we report the first cloned and molecularly characterized five genes coding for the maize putative homologs of ORC subunits ZmORC1, ZmORC2, ZmORC3, ZmORC4 and ZmORC5. Their ***expression*** ***profiles*** in tissues with ***different*** cell-dividing ***activities*** are compatible with a role in DNA replication. Based on the potential of ORC-homologous maize proteins to bind each other in yeast, we propose a model for their possible assembly within a maize ORC. The isolation and mol. characterization of an ORC4-homologous gene from maize argues that, in its evolution, Arabidopsis may have lost the homologous ORC4 gene.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 74 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:222405 CAPLUS <<LOGINID::20100206>>
DN 138:201726
TI Visualization by comprehensive microarray analysis of gene expression programs during transdifferentiation of mesophyll cells into xylem cells
AU Demura, Taku; Tashiro, Gen; Horiguchi, Gorou; Kishimoto, Naoki; Kubo, Minoru; Matsuoka, Naoko; Minami, Atsushi; Nagata-Hiwatashi, Miyo; Nakamura, Keiko; Okamura, Yoshimichi; Sassa, Naomi; Suzuki, Shinsuke; Yazaki, Junshi; Kikuchi, Shoshi; Fukuda, Hiroo
CS Plant Science Center, RIKEN, Yokohama, 230-0045, Japan
SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(24), 15794-15799 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal

LA English
AB Plants have a unique transdifferentiation mechanism by which differentiated cells can initiate a new program of differentiation. A comprehensive anal. of gene expression in an in vitro zinnia (Zinnia elegans) culture model system was used to gather fundamental information about the gene regulation underlying the transdifferentiation of plant cells. In this model, photosynthetic mesophyll cells isolated from zinnia leaves transdifferentiate into xylem cells in a morphogenic process characterized by features such as secondary-wall formation and programmed cell death. More than 8000 zinnia cDNA clones were isolated from an equalized cDNA library prepd. from cultured cells transdifferentiating into xylem cells. Microarray anal. using these cDNAs revealed several types of unique gene regulation patterns, including: the transient expression of a set of genes during cell isolation, presumably induced by wounding; a rapid redn. in the expression of photosynthetic genes and the rapid induction of protein synthesis-assocd. genes during the first stage; the preferential induction of auxin-related genes during the subsequent stage; and the transient induction of genes closely assocd. with particular morphogenetic events, including cell-wall formation and degrdn. and programmed cell death during the final stage. This anal. also revealed a no. of previously uncharacterized genes encoding proteins that function in signal transduction, such as protein kinases and transcription factors that are expressed in a stage-specific manner. These findings provide new clues to the mol. mechanisms of both plant transdifferentiation and wood formation. The sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AB091070-AB091078 and AU285055-AU294769. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 75 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:212043 CAPLUS <<LOGINID::20100206>>
DN 138:383344
TI Gene expression profiles of nondiabetic and diabetic obese mice suggest a role of hepatic lipogenic capacity in diabetes susceptibility
AU Lan, Hong; Rabaglia, Mary E.; Stoehr, Jonathan P.; Nadler, Samuel T.; Schueler, Kathryn L.; Zou, Fei; Yandell, Brian S.; Attie, Alan D.
CS Department of Biochemistry, University of Wisconsin, Madison, WI, 53706, USA
SO Diabetes (2003), 52(3), 688-700 CODEN: DIAEAZ; ISSN: 0012-1797
PB American Diabetes Association
DT Journal
LA English
AB Obesity is a strong risk factor for the development of type 2 diabetes. The authors have previously reported that in adipose tissue of obese (ob/ob) mice, the expression of adipogenic genes is decreased. When made genetically obese, the BTBR mouse strain is diabetes susceptible and the C57BL/6J (B6) strain is diabetes resistant. The authors used DNA microarrays and RT-PCR to compare the gene expression in BTBR-ob/ob vs. B6-ob/ob mice in adipose tissue, liver, skeletal muscle, and pancreatic islets. The authors' results show: (1) there is an increased expression of genes involved in inflammation in adipose tissue of diabetic mice; (2) lipogenic gene expression was lower in adipose tissue of diabetes-susceptible mice, and it continued to decrease with the development of diabetes, compared with diabetes-resistant obese mice; (3) hepatic expression of lipogenic enzymes was increased and the hepatic triglyceride content was greatly elevated in diabetes-resistant obese mice; (4) hepatic expression of gluconeogenic genes was suppressed at the prediabetic stage but not at the onset of diabetes; and (5) genes normally not expressed in skeletal muscle and pancreatic islets were expressed in these tissues in the diabetic mice. The authors propose that increased hepatic lipogenic capacity protects the B6-ob/ob mice from the development of type 2 diabetes.
OSC.G 61 THERE ARE 61 CAPLUS RECORDS THAT CITE THIS RECORD (61 CITINGS)
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 76 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:193410 CAPLUS <<LOGINID::20100206>>
DN 138:364165
TI Insect resistance to Bacillus thuringiensis: Alterations in the Indian meal moth larval gut proteome
AU Candas, Mehmet; Loseva, Olga; Oppert, Brenda; Kosaraju, Pradeepa; Bulla, Lee A., Jr.
CS Biological Targets, Inc., Tioga, TX, 76271, USA
SO Molecular and Cellular Proteomics (2003), 2(1), 19-28
CODEN: MCPOBS; ISSN: 1535-9476
PB American Society for Biochemistry and Molecular Biology, Inc.
DT Journal
LA English
AB Insect resistance to the Cry toxins of Bacillus thuringiensis (Bt) has been examd. previously using a no. of traditional biochem. and mol. techniques. In this study, we utilized a ***proteomic*** approach involving two-dimensional ***differential*** gel electrophoresis, mass spectrometry, and function-based ***activity*** profiling to examine changes in the gut proteins from the larvae of an Indian meal moth (IMM, Plodia interpunctella) colony exhibiting resistance to Bt. We found a no. of changes in the levels of certain specific midgut proteins that indicate increased glutathione utilization, elevation in oxidative metab., and differential maintenance of energy balance within the midgut epithelial cells of the Bt-resistant IMM larva. Addnl., the electrophoretic migration pattern of a low mol. mass acidic protein, which apparently is an ortholog of F1F0-ATPase, was considerably altered in the Bt-resistant insect indicating that variations in amino acid content or modifications of certain proteins also are important components of the resistance phenomenon in the IMM. Furthermore, there was a dramatic decrease in the level of chymotrypsin-like proteinase in the midgut of the Bt-resistant larva, signifying that redn. of chymotrypsin activity, and subsequently decreased activation of Cry toxin in the insect midgut, is an important factor in the resistant state of the IMM. The proteomic anal. of larval gut proteins utilized in this study provides a useful approach for consolidating protein changes and physiol. events assocd. with insect resistance to Bt. Our results support the hypothesis that physiol. adaptation of insects and resistance to Bt is multifaceted, including protein modification and changes in the synthesis of specific larval gut proteins. We believe that increased oxidative metab. may be an adaptive response of insects that undergo survival challenge and that it could mediate detoxification as well as higher rates of generalized and localized mutations that enhance their resistance and provide survival advantage.
OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (28 CITINGS)
RE.CNT 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 77 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:187091 CAPLUS <<LOGINID::20100206>>
DN 138:219713
TI Differentially expressed gene expression profiles in human glomerular diseases
IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.
SO PCT Int. Appl., 781 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ----------
PI WO 2003016476 A2 20030227 WO 2002-XH25766 20020814
WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG WO 2003016476 A2 20030227 WO 2002-US25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814
AB The present invention is based on the elucidation of global changes in gene expression in peripheral blood leukocytes (PBL) of patients with glomerular diseases exhibiting different types of clin. and pathol. features of glomerular nephropathy as compared to normal PBL as well as the identification of individual genes that are differently expressed in PBL of patients with glomerular diseases. The genes and gene expression information may be used as markers for the diagnosis of disease subtype, such as IgA nephropathy, Minimal Change nephrotic syndrome, antineutrophil cytoplasmic antibody-assocd. glomerulonephritis (ANCA), focal segmental glomerulosclerosis (FSGS), and lupus nephritis. The genes may also be used as markers to evaluate the effects of a candidate drug or agent on tissues, including PBLs, particularly PBLs undergoing activation or PBLs from a patient with glomerular disease. Differential expression of genes between PBLs from patients with glomerular disease and normal PBL samples was detd. using the Affymetrix 42K human gene chip set. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 78 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:187090 CAPLUS <<LOGINID::20100206>>
DN 138:219712
TI Differentially expressed gene expression profiles in human glomerular diseases
IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.
SO PCT Int. Appl., 781 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 2003016476 A2 20030227 WO 2002-XG25766 20020814
WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG WO 2003016476 A2 20030227 WO 2002-US25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814
AB The present invention is based on the elucidation of global changes in gene expression in peripheral blood leukocytes (PBL) of patients with glomerular diseases exhibiting different types of clin. and pathol. features of glomerular nephropathy as compared to normal PBL as well as the identification of individual genes that are differently expressed in PBL of patients with glomerular diseases. The genes and gene expression information may be used as markers for the diagnosis of disease subtype, such as IgA nephropathy, Minimal Change nephrotic syndrome, antineutrophil cytoplasmic antibody-assocd. glomerulonephritis (ANCA), focal segmental glomerulosclerosis (FSGS), and lupus nephritis. The genes may also be used as markers to evaluate the effects of a candidate drug or agent on tissues, including PBLs, particularly PBLs undergoing activation or PBLs from a patient with glomerular disease. Differential expression of genes between PBLs from patients with glomerular disease and normal PBL samples was detd. using the Affymetrix 42K human gene chip set. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 79 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2003:187089 CAPLUS <<LOGINID::20100206>>
DN 138:219711
TI Differentially expressed gene expression profiles in human glomerular diseases
IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.
SO PCT Int. Appl., 781 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003016476 A2 20030227 WO 2002-XP25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG WO 2003016476 A2 20030227 WO 2002-US25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814
AB The present invention is based on the elucidation of global changes in gene expression in peripheral blood leukocytes (PBL) of patients with glomerular diseases exhibiting different types of clin. and pathol. features of glomerular nephropathy as compared to normal PBL as well as the identification of individual genes that are differently expressed in PBL of patients with glomerular diseases. The genes and gene expression information may be used as markers for the diagnosis of disease subtype, such as IgA nephropathy, Minimal Change nephrotic syndrome, antineutrophil cytoplasmic antibody-assocd. glomerulonephritis (ANCA), focal segmental glomerulosclerosis (FSGS), and lupus nephritis. The genes may also be used as markers to evaluate the effects of a candidate drug or agent on tissues, including PBLs, particularly PBLs undergoing activation or PBLs from a patient with glomerular disease. Differential expression of genes between PBLs from patients with glomerular disease and normal PBL samples was detd. using the Affymetrix 42K human gene chip set. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 80 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:187088 CAPLUS <<LOGINID::20100206>>
DN 138:219710
TI Differentially expressed gene expression profiles in human glomerular diseases
IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.
SO PCT Int. Appl., 781 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003016476 A2 20030227 WO 2002-XP25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814
AB The present invention is based on the elucidation of global changes in gene expression in peripheral blood leukocytes (PBL) of patients with glomerular diseases exhibiting different types of clin. and pathol. features of glomerular nephropathy as compared to normal PBL as well as the identification of individual genes that are differently expressed in PBL of patients with glomerular diseases. The genes and gene expression information may be used as markers for the diagnosis of disease subtype, such as IgA nephropathy, Minimal Change nephrotic syndrome, antineutrophil cytoplasmic antibody-assocd. glomerulonephritis (ANCA), focal segmental glomerulosclerosis (FSGS), and lupus nephritis. The genes may also be used as markers to evaluate the effects of a candidate drug or agent on tissues, including PBLs, particularly PBLs undergoing activation or PBLs from a patient with glomerular disease. Differential expression of genes between PBLs from patients with glomerular disease and normal PBL samples was detd. using the Affymetrix 42K human gene chip set. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 81 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:187087 CAPLUS <<LOGINID::20100206>>
DN 138:219709
TI Differentially expressed gene expression profiles in human glomerular diseases

IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.
SO PCT Int. Appl., 781 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------

PI WO 2003016476 A2 20030227 WO 2002-XD25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG WO 2003016476 A2 20030227 WO 2002-US25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814

AB The present invention is based on the elucidation of global changes in gene expression in peripheral blood leukocytes (PBL) of patients with glomerular diseases exhibiting different types of clin. and pathol. features of glomerular nephropathy as compared to normal PBL as well as the identification of individual genes that are differently expressed in PBL of patients with glomerular diseases. The genes and gene expression information may be used as markers for the diagnosis of disease subtype, such as IgA nephropathy, Minimal Change nephrotic syndrome, antineutrophil cytoplasmic antibody-assocd. glomerulonephritis (ANCA), focal segmental glomerulosclerosis (FSGS), and lupus nephritis. The genes may also be used as markers to evaluate the effects of a candidate drug or agent on tissues, including PBLs, particularly PBLs undergoing activation or PBLs from a patient with glomerular disease. Differential expression of genes between PBLs from patients with glomerular disease and normal PBL samples was detd. using the Affymetrix 42K human gene chip set. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 82 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:187086 CAPLUS <<LOGINID::20100206>>
DN 138:185696
TI Differentially expressed gene expression profiles in human glomerular diseases
IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.
SO PCT Int. Appl., 781 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------

PI WO 2003016476 A2 20030227 WO 2002-XC25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG WO 2003016476 A2 20030227 WO 2002-US25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814

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L12 ANSWER 83 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:187085 CAPLUS <<LOGINID::20100206>>
DN 138:185695
TI Differentially expressed gene expression profiles in human glomerular diseases
IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.

SO PCT Int. Appl., 781 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2003016476 A2 20030227 WO 2002-XB25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG WO 2003016476 A2 20030227 WO 2002-US25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814
AB The present invention is based on the elucidation of global changes in gene expression in peripheral blood leukocytes (PBL) of patients with glomerular diseases exhibiting different types of clin. and pathol. features of glomerular nephropathy as compared to normal PBL as well as the identification of individual genes that are differently expressed in PBL of patients with glomerular diseases. The genes and gene expression information may be used as markers for the diagnosis of disease subtype, such as IgA nephropathy, Minimal Change nephrotic syndrome, antineutrophil cytoplasmic antibody-assocd. glomerulonephritis (ANCA), focal segmental glomerulosclerosis (FSGS), and lupus nephritis. The genes may also be used as markers to evaluate the effects of a candidate drug or agent on tissues, including PBLs, particularly PBLs undergoing activation or PBLs from a patient with glomerular disease. Differential expression of genes between PBLs from patients with glomerular disease and normal PBL samples was detd. using the Affymetrix 42K human gene chip set. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 84 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:187084 CAPLUS <<LOGINID::20100206>>
DN 138:185694
TI Differentially expressed gene expression profiles in human glomerular diseases
IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.
SO PCT Int. Appl., 781 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2003016476 A2 20030227 WO 2002-XA25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814
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L12 ANSWER 85 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:173640 CAPLUS <<LOGINID::20100206>>
DN 138:219717
TI Genes that are differentially regulated under hypoxic conditions and their diagnostic and therapeutic uses
IN Kingsman, Susan Mary; White, Jonathan; Ward, Neil Raymond; Harris, Robert Alan; Naylor, Stuart; Mundy, Christopher Robert
PA Oxford Biomedica (UK) Limited, UK
SO PCT Int. Appl., 424 pp. CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE

PI WO 2003018621 A2 20030306 WO 2002-GB3892 20020823
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
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AU 2002313559 A1 20030310 AU 2002-313559 20020823
PRAI GB 2001-20558 A 20010823
GB 2001-24037 A 20011005
WO 2002-GB3892 W 20020823

AB This invention relates to novel genes and gene products that are implicated in certain disease states. The Smartomics method was utilized to improve the discovery of genes activated or repressed in response to hypoxia in primary human macrophages. This involves augmenting the natural response to hypoxia by exptl. introducing key regulators of the hypoxia response, namely hypoxia-inducible factor 1 (HIF-1) and HIF-2 (also known as EPAS1), into a population of primary human macrophages and comparing gene expression in these cells with that in control cells. The expression of certain polypeptides was induced under conditions of hypoxia, as mimicked by adenoviral overexpression of HIF-1.alpha. or EPAS1. The expression of certain of these hypoxia-regulated genes is responsive to cytokines and other mols., including tumor necrosis factor .alpha., interleukin 1.beta. (IL-1.beta.), lipopolysaccharide and .gamma.-interferon, IL-12, IL-15, IL-17, IL-13, IL-4, IL-10, and superoxide. Differential expression is also noted in various cell types and tissues, and in tumors, chronic obstructive pulmonary disease, and artherosclerosis. Thus, the invention provides for the diagnosis and therapeutic targets for hypoxia-regulated conditions. Also, methods for the detection of mutations or abnormal expression levels of the transcripts and their encoded protein products are provided.

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L12 ANSWER 86 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2003:154556 CAPLUS <<LOGINID::20100206>>

DN 138:168236

TI Differentially expressed gene expression profiles in human glomerular diseases

IN Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun

PA Gene Logic, Inc., USA; University of North Carolina at Chapel Hill; Japan Tobacco, Inc.

SO PCT Int. Appl., 781 pp. CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 9 PATENT NO. KIND DATE APPLICATION NO. DATE

PI WO 2003016476 A2 20030227 WO 2002-US25766 20020814
WO 2003016476 A3 20030508
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RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AB This invention relates to novel genes and gene products that are implicated in certain disease states. The Smartomics method was utilized to improve the discovery of genes activated or repressed in response to hypoxia in primary human macrophages. This involves augmenting the natural response to hypoxia by exptl. introducing key regulators of the hypoxia response, namely hypoxia-inducible factor 1 (HIF-1) and HIF-2 (also known as EPAS1), into a population of primary human macrophages and comparing gene expression in these cells with that in control cells. The expression of certain polypeptides was induced under conditions of hypoxia, as mimicked by adenoviral overexpression of HIF-1.alpha. or EPAS1. The expression of certain of these hypoxia-regulated genes is responsive to cytokines and other mols., including tumor necrosis factor .alpha., interleukin 1.beta. (IL-1.beta.), lipopolysaccharide and .gamma.-interferon, IL-12, IL-15, IL-17, IL-13, IL-4, IL-10, and superoxide. Differential expression is also noted in various cell types and tissues, and in tumors, chronic obstructive pulmonary disease, and artherosclerosis. Thus, the invention provides for the diagnosis and therapeutic targets for hypoxia-regulated conditions. Also, methods for the detection of mutations or abnormal expression levels of the transcripts and their encoded protein products are provided.

MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG WO 2003016476 A2 20030227 WO 2002-XF25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG WO 2003016476 A2 20030227 WO 2002-XG25766 20020814 WO 2003016476 A3 20030508 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002324701 A1 20030303 AU 2002-324701 20020814
PRAI US 2001-311837P P 20010814 WO 2002-US25766 20020814

AB The present invention is based on the elucidation of global changes in gene expression in peripheral blood leukocytes (PBL) of patients with glomerular diseases exhibiting different types of clin. and pathol. features of glomerular nephropathy as compared to normal PBL as well as the identification of individual genes that are differently expressed in PBL of patients with glomerular diseases. The genes and gene expression information may be used as markers for the diagnosis of disease subtype, such as IgA nephropathy, Minimal Change nephrotic syndrome, antineutrophil cytoplasmic antibody-associd. glomerulonephritis (ANCA), focal segmental glomerulosclerosis (FSGS), and lupus nephritis. The genes may also be used as markers to evaluate the effects of a candidate drug or agent on tissues, including PBLs, particularly PBLs undergoing activation or PBLs from a patient with glomerular disease. Differential expression of genes between PBLs from patients with glomerular disease and normal PBL samples was detd. using the Affymetrix 42K human gene chip set. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 87 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:133417 CAPLUS <<LOGINID::20100206>>
DN 138:166222
TI Detection of differential expression of protein using gel-free proteomics
IN Brame, Cynthia J.
PA MDS Proteomics, Inc., Can.
SO PCT Int. Appl., 80 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003014302 A2 20030220 WO 2002-US24650 20020802 WO 2003014302 A3 20031224 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002321899 A1 20030224 AU 2002-321899 20020802 US 20030119062 A1 20030626 US 2002-211945 20020802
PRAI US 2001-309903P P 20010803 WO 2002-US24650 W 20020802

AB Methods and reagents for analyzing differential expression and/or abundance of distinct membrane-assocd. polypeptide samples, particularly integral membrane polypeptide samples are provided. Also provides are methods for screening pharmaceutical components that can affect expression or abundance of certain membrane-assocd. polypeptides; methods for identification of drug targets; and methods for diagnosis of certain disease states. Business methods for conducting a pharmaceutical business based on the result of using the above methods are also provided.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L12 ANSWER 88 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:129938 CAPLUS <<LOGINID::20100206>>
DN 138:318572
TI Differential mechanisms of constitutive Akt/PKB activation and its influence on gene expression in pancreatic cancer cells
AU Matsumoto, Joe; Kaneda, Masako; Tada, Mitsuhiro; Hamada, Jun-ichi; Okushiba, Shunichi; Kondo, Satoshi; Katoh, Hiroyuki; Moriuchi, Tetsuya
CS Division of Cancer-related Genes, Institute for Genetic Medicine, Hokkaido University, Sapporo, 060-0815, Japan
SO Japanese Journal of Cancer Research (2002), 93(12), 1317-1326 CODEN: JJCREP; ISSN: 0910-5050
PB Japanese Cancer Association
DT Journal
LA English
AB Activated Akt/protein kinase B transmits oncogenic signals leading to inhibition of apoptosis, cellular proliferation, and tolerance to hypoxia. Presently, mutational inactivation of PTEN and activation of Ras are considered to be the major causes of Akt activation. Here the authors report differential mechanisms of constitutive Akt activation in 4 human pancreatic cancer cell

lines (KMP-3, KMP-4, PCI-66, and PCI-68). These 4 cell lines displayed phosphorylation and functional activation of Akt both in the presence and absence of serum, while three control cell lines (PCI-79, KMP-8, and PSN-1) did so only in the presence of serum in culture. All the 7 cell lines harbored K-Ras activated by mutations at codon 12 resulting in MAP kinase kinase (MEK1/2) phosphorylation, and all except one (KMP-8) had p53 mutations, indicating that these mutations are not sufficient for constitutive Akt activation. KMP-3 and KMP-4 had lost PTEN function owing to loss of expression or a mutation, but PCI-66 and PCI-68 retained wild-type PTEN. Phosphorylation of Akt was inhibited by the phosphatidylinositol-3-kinase (PI3K) inhibitor LY294002 and the tyrosine kinase inhibitor genistein in KMP-3 and KMP-4 cells, indicating that upstream signals are required for Akt activation in these two cell lines. In contrast, neither LY294002 nor genistein inhibited Akt activation in PCI-66 and PCI-68 cells, indicating the involvement of another unknown mechanism of Akt activation independent of PI3K-mediated signaling to Akt. Irresp. of the differential mechanisms, the 4 cell lines showed similar mRNA expression patterns of 49 genes assessed by cDNA array as compared to the 3 cell lines without Akt activation, suggesting that the mechanisms have the same consequences on the downstream signaling of the constitutive Akt activation.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 89 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:128290 CAPLUS <<LOGINID::20100206>>
DN 138:236854
TI Gene profiling approach to establish the molecular bases for partial versus full activation of naive CD8 T lymphocytes
AU Verdeil, Gregory; Puthier, Denis; Nguyen, Catherine; Schmitt-Verhulst, Anne-Marie; Auphan-Anezin, Nathalie
CS Centre d'Immunologie de Marseille-Luminy, CNRS-INSERM-Univ. de la Mediterranee, Marseille-Luminy, Fr.
SO Annals of the New York Academy of Sciences (2002), 975(Microarrays, Immune Responses, and Vaccines), 68-76
CODEN: ANYAA9; ISSN: 0077-8923
PB New York Academy of Sciences
DT Journal
LA English
AB When initial antigen encounter involves optimal antigenic and costimulatory stimuli, naive CD8 T cells undergo a developmental program that leads to their activation, expansion and acquisition of effector functions (including prodn. of IL-2, IFN.gamma. and expression of cytolytic effector mols.). A subset of the activated CD8 T cells thrives as long-lived memory cells. Encounter of tissue-associd., and in particular tumor-associd. antigen, may often be suboptimal in terms of antigenicity and costimulation, however. We previously developed a model of naive CD8 T cells from transgenic mice expressing an alloreactive TCR for which a mutant alloantigen behaved as a partial agonist, inducing only some of the effector functions induced by the native alloantigen. To ascertain the mol. bases for the establishment of divergent fates within the same naive CD8 T cells, we have used cDNA microarrays to monitor sequential gene expression patterns in conditions of full or partial response of these naive CD8 T cells. Of the 5000 different genes monitored on the array, 18% showed changes in expression in activated vs. naive CD8 T cells, independent of whether stimulation was with full or partial agonist. These included antigen-induced upregulated as well as downregulated genes. Clusters of genes that were differentially expressed were also identified, being either (i) weakly vs. strongly, or (ii) transiently vs. stably expressed in response to partial and full agonist, resp. They included (i) genes encoding costimulatory mols. and (ii) genes controlling cytolytic function, cytokine prodn., and chemokines. Therefore, the cDNA microarray approach was a sensitive tool to provide an exhaustive picture of T cell ***activation*** as it could discriminate quant., qual. and dynamic ***differences*** in mRNA ***expression*** ***profiles*** between fully or partially ***activated*** T cells.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 90 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:102658 CAPLUS <<LOGINID::20100206>>
DN 138:236717
TI Expression Patterns of Phenotypic Markers on Lymphocytes from Human Immunodeficiency Virus Type 2-Infected Baboons
AU Locher, Christopher P.; Fujimura, Sue; Murthy, Krishna K.; Brasky, Kathleen; Leland, Michelle; Levy, Jay A.
CS Division of Vaccines, Maxygen, Redwood City, CA, 94063, USA
SO AIDS Research and Human Retroviruses (2003), 19(1), 31-40 CODEN: ARHRE7; ISSN: 0889-2229
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB The development of AIDS in HIV-1-infected humans is assocd. with profound ***changes*** in the ***expression*** ***patterns*** of lymphocyte phenotypic markers assocd. with increased immune ***activation*** and with decreased recall immune responses. In assessing these immunol. ***changes*** in an animal model, the authors characterized the ***expression*** ***patterns*** of immune ***activation*** markers on lymphocyte subsets during the acute, chronic, and end stages of HIV-2 infection in baboons. Using flow cytometry, the authors identified 21 human-specific monoclonal antibodies that were cross-reactive with baboon lymphocytes; however, expression of only 2 of these markers was altered significantly after HIV-2 infection. The authors found an increase in baboon class II antigen (as measured by anti-HLA-DR) in the CD4+ T cell subset within 8 wk of infection. Moreover, after 1 yr of infection, CD11b was down-regulated on CD8+ T lymphocytes. This down-regulation of CD11b was consistently obsd. in all of the groups of baboons that were chronically infected with three different HIV-2 isolates. In addn., the authors found substantial down-regulation of the interleukin 2 receptor (CD25) and upregulation of class II antigen on CD8+ lymphocytes in a baboon with an AIDS-like disease. These and other phenotypic markers of immune activation may facilitate characterization of the immunopathogenesis of AIDS in nonhuman primate animal models.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 91 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:96560 CAPLUS <<LOGINID::20100206>>
DN 139:207206

TI Changes in gene expression profile induced by the anticancer agent Aplidine in Molt-4 leukemic cell lines
AU Marchini, S.; Chiorino, G.; Fairdoth, G. T.; D'Incalci, M.
CS Department of Oncology, Istituto di Ricerche Farmacologiche "Mario Negri", Milan, Italy
SO Journal of Biological Regulators and Homeostatic Agents (2002), 16(3), 241-248 CODEN: JBRAER; ISSN: 0393-974X
PB Wichtig Editore
DT Journal
LA English
AB Microarray technique was employed to study differences in gene expression profile induced by Aplidine treatment in the Molt-4 human leukemic T cell line. Aplidine is a novel marine compd. purified from caribbean tunicate (sea squirt) Aplidium albicans. Despite promising antitumor activity, few data are available on its mechanism of action. Exponentially growing cells were treated with Aplidine concns. close to its IC50 for 1 h and RNA samples collected after 0.5, 1, 6 and 24 h of recovery in drug free medium. The 32P labeled cDNAs were hybridized against Atlas Human Cancer arrays onto which 588 cDNAs were spotted. Genes involved in different cellular pathways, (such as growth factors, signal transduction or transcription factors) were found modulated by the drug. Even if the data obtained in the present study cannot be conclusive, several hypothesis on Aplidine's mechanism of action are indicated that will be the subject of future studies.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 92 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:81393 CAPLUS <<LOGINID::20100206>>
DN 138:334396
TI Poplar potassium transporters capable of controlling K+ homeostasis and K+-dependent xylogenesis
AU Langer, Katharina; Ache, Peter; Geiger, Dietmar; Stinzing, Andrea; Arend, Matthias; Wind, Christa; Regan, Sharon; Fromm, Joerg; Hedrich, Rainer
CS Julius-von-Sachs-Institut, Molekulare Pflanzenphysiologie und Biophysik, Universitaet Wuerzburg, Wuerzburg, 97082, Germany
SO Plant Journal (2002), 32(6), 997-1009 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB The cambial K+ content of poplar increases during the growth period in a K+ supply dependent manner. Upon K+ starvation or application of tetraethylammoniumchloride (TEA+), a K+ channel blocker, the av. vessel lumen and expansion zone area were significantly reduced. In a search for the mol. basis of potassium-dependent xylogenesis in poplar, K+ transporters homologous to those of known function in Arabidopsis phloem- and xylem-physiol. were isolated from a poplar wood EST library. The expression profile of three distinct K+ channel types and one K+ transporter, Populus tremula K+ uptake transporter 1 (PtKUP1), was analyzed by quant. RT-PCR. Thereby, the authors found P. tremula outward rectifying K+ channel (PTORK) and P. tremula K+ channel 2 (PTK2) correlated with the seasonal wood prodn. K+ transporter P. tremula 1 (KPT1) was predominantly found in guard cells. Following the heterologous expression in Xenopus oocytes the biophys. properties of the different channels were detd. PTORK, upon membrane de-polarization mediates potassium release. PTK2 is almost voltage independent, carrying inward K+ flux at hyperpolarized potential and K+ release upon de-polarization. PtKUP1 was expressed in a K+ uptake-deficient Escherichia coli strain, where this K+ transporter rescued K+-dependent growth, in order to link the different K+ transporters to the cambial ***activity*** and wood prodn., we compared the ***expression*** ***profiles** to seasonal ***changes*** in the K+ content of the bark as well as xylem vessel diam. Thereby, the authors found PTORK and PTK2 transcripts to follow the annual K+ variations in poplar branches. PtKUP1 was expressed at a low level throughout the year, suggesting a housekeeping function. From these data, it was concluded that K+ channels are involved in the regulation of K+-dependent wood prodn.
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)
RE.CNT 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 93 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:50697 CAPLUS <<LOGINID::20100206>>
DN 139:46291
TI Discriminating two classes of toxicants through expression analysis of HepG2 cells with DNA arrays
AU Hong, Y.; Muller, U. R.; Lai, F.
CS Science and Technology Division, Corning Incorporated, Corning, NY, 14831, USA
SO Toxicology in Vitro (2003), 17(1), 85-92 CODEN: TIVIEQ; ISSN: 0887-2333
PB Elsevier Science Ltd.
DT Journal
LA English
AB Microarray technol. provides a rapid and cost-effective method to assoc. specific cellular responses with unique gene expression patterns. If characteristic expression patterns of a small no. of genes could be assocd. with drug toxicity, this assocn. may be used for toxicity prediction, and thereby to reduce the need for traditional toxicity testing. To test this hypothesis, we have designed an array composed of 92 known human genes of toxicol. interest (including seven housekeeping genes) and eight bacterial controls. HepG2 cells were treated with either ethanol or one of two quinone contg. anticancer drugs, mitomycin C or doxorubicin. RNA was isolated from treated and untreated cells, differentially labeled with fluorescent dyes, and then hybridized to the array. Our results show that the ***expression*** ***patterns*** induced by ethanol and the anticancer ***drugs*** are ***different*** . Both of the anticancer drugs, but not ethanol had a differential effect on the regulation of several genes, including CYP4F2/3, CYP3A3, TNFRSF6 and CHES1, demonstrating that the two drugs might function through a similar mechanism, which differs from that of ethanol. These results suggest that microarray-based expression anal. may offer a rapid and efficient means for assessing drug toxicity.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 94 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:45259 CAPLUS <<LOGINID::20100206>>
DN 139:19923

TI Regulation of Expression of the Phospholipid Hydroperoxide/ Sperm Nucleus Glutathione Peroxidase Gene
AU Borchert, Astrid; Savaskan, Nicolai E.; Kuhn, Hartmut
CS Institute of Biochemistry, Humboldt University Medical School Charite, Berlin, 10117, Germany
SO Journal of Biological Chemistry (2003), 278(4), 2571-2580 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB A sperm nucleus glutathione peroxidase (snGPx), which is closely related to the phospholipid hydroperoxide glutathione peroxidase (phGPx), was recently discovered in late spermatids. Both GPx isoforms originate from a joint ph/snGPx gene, but their N-terminal peptides are encoded by alternative first exons. The expression of the two enzymes is differentially regulated in various cells, but little is known about the regulatory mechanisms. To explore the tissue-specific regulation of expression of the two isoenzymes, we first investigated their tissue distribution. Whereas phGPx is expressed at low levels in many organs, snGPx was only detected in testis, kidney, and in the human embryonic kidney cell line HEK293. Subcellular fractionation studies and immunoelectron microscopy revealed a cytosolic localization. To explore the mechanistic reasons for the ***differential*** ***expression*** ***pattern*** , we first tested the ***activity*** of the putative phGPx and snGPx promoters. The 5'-flanking region of the joint ph/snGPx gene exhibits strong promoter activity. In contrast, the putative snGPx promoter, which comprises 334 bp of intronic sequences, lacks major promoter activity. However, it strongly suppresses the activity of the ph/snGPx promoter. These data suggest neg. regulatory elements in the first intron of the ph/snGPx gene, and DNase protection assays revealed the existence of several protein-binding sites. The corresponding trans-regulatory proteins (SP1, ERG1, GATA1, SREBP1, USF1, and CREBBP1) were identified, and in vivo binding of EGR1 and SREBP1 was shown by chromatin immunopptn. These data indicate for the first time somatic expression of the snGPx and provide evidence for the existence of intronic neg. cis-regulatory elements in the ph/snGPx gene. Our failure to detect an alternative snGPx promoter suggests that transcription of the ph/snGPx gene may be regulated by a joint basic promoter. The decision, which GPx isoform is expressed in a given cell, appears to be made by alternative splicing of a joint primary transcript.
OSC.G 29 THERE ARE 29 CAPLUS RECORDS THAT CITE THIS RECORD (29 CITINGS)
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 95 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:44657 CAPLUS <<LOGINID::20100206>>
DN 138:382156
TI 4-Coumarate:CoA ligase gene family in Rubus idaeus: cDNA structures, evolution, and expression
AU Kumar, Amrita; Ellis, Brian E.
CS Biotechnol. Lab., Fac. Agric. Sci., Univ. British Columbia, Vancouver, BC, V6T 1Z4, Can.
SO Plant Molecular Biology (2003), 51(3), 327-340 CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer Academic Publishers
DT Journal
LA English
AB The enzyme 4-coumarate:CoA ligase (4CL) activates cinnamic acid and its hydroxylated derivs. by forming the corresponding CoA thioesters. These serve as substrates for biosynthesis of phenylpropanoid-derived end-products that are important determinants of fruit quality in raspberry (Rubus idaeus L.). In higher plants, 4CL is typically encoded by a gene family. To investigate the participation of distinct 4CL genes in the process of fruit ripening, we have characterized this gene family in raspberry. By complementing a PCR-based homol. search with low-stringency cDNA library screening, we have isolated three classes of raspberry 4CL cDNAs (Ri4CL1, Ri4CL2, and Ri4CL3). Phylogenetic anal. places the three raspberry 4CL gene family members into two distinct groups, a pattern consistent with an ancient divergence from an ancestral progenitor. Quant. RT-PCR assay reveals a differential pattern of transcription of each of the three genes in various organs, as well as distinct temporal patterns of expression during flower and fruit development. The regulatory elements thus appear to have evolved independently of the genes themselves. Based on phylogenetic classification, ***expression*** ***patterns*** and recombinant protein ***activities*** the ***different*** Ri4CL genes are likely to participate in different biosynthetic pathways leading to the various phenylpropanoid-derived metabolites that help create flavor and color in raspberry fruit.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 96 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:18997 CAPLUS <<LOGINID::20100206>>
DN 138:317270
TI Circadian clock protein KaiC forms ATP-dependent hexameric rings and binds DNA
AU Mori, Tetsuya; Saveliev, Sergei V.; Xu, Yao; Stafford, Walter F.; Cox, Michael M.; Inman, Ross B.; Johnson, Carl H.
CS Department of Biological Sciences, Vanderbilt University, Nashville, TN, 37235, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(26), 17203-17208 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB KaiC from Synechococcus elongatus PCC 7942 (KaiC) is an essential circadian clock protein in cyanobacteria. Previous sequence analyses suggested its inclusion in the RecA/ DnaB superfamily. A characteristic of the proteins of this superfamily is that they form homohexameric complexes that bind DNA. We show here that KaiC also forms ring complexes with a central pore that can be visualized by electron microscopy. A combination of anal. ultracentrifugation and chromatog. analyses demonstrates that these complexes are hexameric. The assocn. of KaiC mols. into hexamers depends on the presence of ATP. The KaiC sequence does not include the obvious DNA-binding motifs found in RecA or DnaB. Nevertheless, KaiC binds forked DNA substrates. These data support the inclusion of KaiC into the RecA/DnaB superfamily and have important implications for enzymic ***activity*** of KaiC in the circadian clock mechanism that regulates global ***changes** in gene ***expression*** ***patterns***
OSC.G 61 THERE ARE 61 CAPLUS RECORDS THAT CITE THIS RECORD (61 CITINGS)
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 97 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:17089 CAPLUS <<LOGINID::20100206>>
DN 138:281897
TI Identification of seed-specific promoter nap300 and its comparison with 7S promoter
AU Zhang, Jingyu; Li, Li; Song, Yanru
CS Key Laboratory of Photosynthesis and Environmental Molecular Physiology, Institute of Botany, Chinese Academy of Sciences, Beijing, 100093, Peop. Rep. China
SO Progress in Natural Science (2002), 12(10), 737-741
CODEN: PNASEA; ISSN: 1002-0071
PB Science in China Press
DT Journal
LA English
AB By fusing seed-specific promoter nap300 with .beta.-glucuronidase gene, it was found that this about 300 bp DNA fragment was sufficient to direct seed-specific gene expression. The substitution mutation in both distB and proxB elements had a little effect on the expression efficiency and almost no effect on the organ-specific expression pattern. In the expt. designed to compare nap300 with 7S promoter, the result showed that tissue specificity for nap300 was higher than that for 7S, and its expression level was lower than 7S's. There was no big ***difference*** in their ***expression*** ***pattern*** , and the maximal ***activity*** stage for the two promoters was identical, which indicated they could be used simultaneously for expressing different foreign genes in seeds.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 98 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:3921 CAPLUS <<LOGINID::20100206>>
DN 138:201716
TI Visualization by comprehensive microarray analysis of gene expression programs during transdifferentiation of mesophyll cells into xylem cells
AU Demura, Taku; Tashiro, Gen; Horiguchi, Gorou; Kishimoto, Naoki; Kubo, Minoru; Matsuoka, Naoko; Minami, Atsushi; Nagata-Hiwatashi, Miyo; Nakamura, Keiko; Okamura, Yoshimichi; Sassa, Naomi; Suzuki, Shinsuke; Yazaki, Junshi; Kikuchi, Shoshi; Fukuda, Hiroo
CS Plant Science Center, RIKEN, Yokohama, 230-0045, Japan
SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(24), 15794-15799 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Plants have a unique transdifferentiation mechanism by which differentiated cells can initiate a new program of differentiation. A comprehensive anal. of gene expression in an in vitro zinnia (Zinnia elegans) culture model system was used to gather fundamental information about the gene regulation underlying the transdifferentiation of plant cells. In this model, photosynthetic mesophyll cells isolated from zinnia leaves transdifferentiate into xylem cells in a morphogenic process characterized by features such as secondary-wall formation and programmed cell death. More than 8000 zinnia cDNA clones were isolated from an equalized cDNA library prepd. from cultured cells transdifferentiating into xylem cells. Microarray anal. using these cDNAs revealed several types of unique gene regulation patterns, including: the transient expression of a set of genes during cell isolation, presumably induced by wounding; a rapid redn. in the expression of photosynthetic genes and the rapid induction of protein synthesis-assocd. genes during the first stage; the preferential induction of auxin-related genes during the subsequent stage; and the transient induction of genes closely assocd. with particular morphogenetic events, including cell-wall formation and degrdn. and programmed cell death during the final stage. This anal. also revealed a no. of previously uncharacterized genes encoding proteins that function in signal transduction, such as protein kinases and transcription factors that are expressed in a stage-specific manner. These findings provide new clues to the mol. mechanisms of both plant transdifferentiation and wood formation. The sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AB091070-AB091078 and AU285055-AU294769. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 99 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:3894 CAPLUS <<LOGINID::20100206>>
DN 138:199477
TI Gene expression profiling of isogenic cells with different TP53 gene dosage reveals numerous genes that are affected by TP53 dosage and identifies CSPG2 as a direct target of p53
AU Yoon, Heejei; Liyanarachchi, Sandya; Wright, Fred A.; Davuluri, Ramana; Lockman, Janet C.; De la Chapelle, Albert; Pellegata, Natalia S.
CS Human Cancer Genetics Program, Comprehensive Cancer Center, Ohio State University, Columbus, OH, 43210, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(24), 15632-15637 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB TP53 does not fully comply with the Knudson model in that a redn. of constitutional expression of p53 may be sufficient for tumor predisposition. This finding suggests a gene-dosage effect for p53 function. To det. whether TP53 gene dosage affects the transcriptional regulation of target genes, we performed oligonucleotide-array gene expression anal. by using human cells with wild-type p53 (p53 +/+), or with one (p53 +/-), or both (p53 -/-) TP53 alleles disrupted by homologous recombination. We identified 35 genes whose expression is significantly correlated to the dosage of TP53. These genes are involved in a variety of cellular processes including signal transduction, cell adhesion, and transcription regulation. Several of them are involved in neurogenesis and neural crest migration, developmental processes in which p53 is known to play a role. Motif search anal. revealed that of the genes highly expressed in p53 +/+ and +/- cells, several contain a putative p53 consensus binding site (bs), suggesting that they could be directly regulated by p53. Among those genes, we chose CSPG2 (which encodes versican) for further study because it contains a bona fide p53 bs in its first intron and its expression highly correlates with TP53 dosage. By using in vitro and in vivo assays, we showed CSPG2 to be directly transactivated by p53. In conclusion, we developed a strategy to demonstrate that many genes are affected by TP53 gene dosage for their expression. We report several candidate

genes as potential downstream targets of p53 in nonstressed cells. Among them, CSPG2 is validated as being directly transactivated by p53. Our method provides a useful tool to elucidate addnl. mechanisms by which p53 exerts its functions.
OSC.G 33 THERE ARE 33 CAPLUS RECORDS THAT CITE THIS RECORD (33 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 100 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:3561 CAPLUS <<LOGINID::20100206>>
DN 138:235293
TI Analysis of the PC12 cell transcriptome after differentiation with pituitary adenylate cyclase-activating polypeptide (PACAP)
AU Vaudry, David; Chen, Yun; Ravni, Aurelia; Hamelink, Carol; Elkahloun, Abdel G.; Eiden, Lee E.
CS Section on Molecular Neuroscience, Laboratory of Cellular and Molecular Regulation, National Institute of Mental Health, NIH, Bethesda, MD, USA
SO Journal of Neurochemistry (2002), 83(6), 1272-1284
CODEN: JONRA9; ISSN: 0022-3042
PB Blackwell Science Ltd.
DT Journal
LA English
AB Pituitary adenylate cyclase-activating polypeptide (PACAP) promotes neurite outgrowth and inhibits proliferation of rat pheochromocytoma (PC12) cells. Characterizing the PACAP-differentiated PC12 cell transcriptome should provide genetic insight into how these processes occur in these cells, and in neuronal precursors in vivo. For this purpose, RNA samples were collected from PC12 cells before or after a 6-h treatment with PACAP, from which a labeled cDNA was hybridized to a high-d. cDNA array contg. 15 365 genes. The genomic response to PACAP involves at least 73 genes. Among the genes differentially expressed in the presence of PACAP, 71% were up regulated, and 29% down regulated, 2-fold or more. Sixty-six percent of the messages affected by PACAP code for functionally categorized proteins, most not previously known to be regulated during PC12 cell differentiation. PACAP has been shown to induce PC12 cell neurite outgrowth through the mitogen-activated protein kinase kinase (MEK) pathway independently of protein kinase A (PKA). Therefore treatments were conducted in the absence or presence of the PKA inhibitor H89, or the MEK inhibitor U0126 in order to identify subsets of genes involved in specific aspects of PC12 cell differentiation. Co-treatment of PC12 cells with PACAP plus H89 revealed a cluster of five genes specifically regulated through the PKA pathway and co-treatment of the cells with PACAP and U0126 revealed a cluster of 13 messages specifically activated through the MEK pathway. Many of the known genes regulated by PACAP have been assocd. with neuritogenesis (i.e. villin 2 or annexin A2) or cell growth (i.e. growth arrest specific 1 or cyclin B2). Thus, some of the expressed sequence tags (ESTs) that exhibit the same regulation pattern (i.e. AU016391 or AW552690) may also be involved in the neuritogenic and anti-mitogenic effects of PACAP in PC12 cells. Among the 73 PACAP regulated genes, 10 are disqualified on pharmacol. grounds as actors in PACAP-mediated neurite outgrowth or growth arrest, leaving 63 new PACAP-regulated genes implicated in neuronal differentiation. Thirteen of these are candidates for mediating ERK-dependent neurite outgrowth, and 47 are possibly involved in the ERK-independent growth arrest induced by PACAP.
OSC.G 32 THERE ARE 32 CAPLUS RECORDS THAT CITE THIS RECORD (32 CITINGS)
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 101 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:975050 CAPLUS <<LOGINID::20100206>>
DN 138:351647
TI Regulation of TonEBP transcriptional activator in MDCK cells following changes in ambient tonicity
AU Neuhofer, Wolfgang; Woo, Seung Kyoon; Na, Ki Young; Grunbein, Rita; Park, Won Kun; Nahm, Ohnn; Beck, Franz-X.; Kwon, H. Moo
CS Physiologisches Institut der Universitat Munchen, Munich, D-80336, Germany
SO American Journal of Physiology (2002), 283(6, Pt. 1), C1604-C1611 CODEN: AJPHAP; ISSN: 0002-9513
PB American Physiological Society
DT Journal
LA English
AB In response to ambient hypertonicity, TonEBP (tonicity-responsive enhancer binding protein) stimulates certain genes including those encoding cytokines, transporters for org. solutes, and a mol. chaperone. TonEBP is regulated in a bidirectional manner, upregulated by an increase in ambient tonicity while downregulated by a decrease. To investigate the role of intracellular ionic strength in the activity of TonEBP, we subjected Madin-Darby canine kidney cells to a variety of conditions. Electron microprobe anal. was performed to measure intracellular electrolytes. Under conditions in which changes in cell vol. were similar, TonEBP activity correlated with the intracellular ionic strength regardless of the external tonicity. On the other hand, inhibition of the Na+/K+-ATPase and high external K+ concn. led to a decreased activity of TonEBP despite a marked increase in the intracellular ionic strength. Because isotonic swelling is known to occur under these conditions, these data suggest that diln. of the cytoplasmic constituents inhibits the activity of TonEBP. We conclude that intracellular ionic strength and water content are major factors that det. the activity of TonEBP.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 102 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:973962 CAPLUS <<LOGINID::20100206>>
DN 138:215044
TI Gene expression profile after peroxisome proliferator activator receptor-.gamma. ligand administration in dextran sodium sulfate mice
AU Nakajima, Atsushi; Wada, Koichiro; Katayama, Kazufumi; Saubermann, Lawrence; Osawa, Emi; Nagase, Hajime; Ueno, Norio; Matsuhashi, Nobuyuki; Aburatani, Hiroyuki
CS Third Department of Internal Medicine, Yokohama City University School of Medicine, Kanazawa-ku, Yokohama, 236-0004, Japan
SO Journal of Gastroenterology (2002), 37(Suppl. 14), 62-66
CODEN: JOGAET; ISSN: 0944-1174
PB Springer-Verlag Tokyo
DT Journal
LA English
AB Peroxisome proliferator activator receptor-gamma (PPAR.gamma.) is a member of the nuclear receptor superfamily. Ligands of PPAR.gamma., thiazolidione derivs., have been

reported to be the one of the candidates for the treatment of inflammatory bowel disease (IBD). Given the fact that PPAR.gamma. is a transcription regulator, expression pharmacogenomics, including ***differential*** gene ***expression*** ***profiling*** of ***drug*** responses in a colitis model, is thought to be a useful approach for finding relevant genes that can serve as the target for new drug treatment of IBD. We performed a global anal. for differential gene expression of the intestine in a dextran sodium sulfate (DSS) colitis mouse model following PPAR.gamma. ligand administration. By applying a high-d. oligonucleotide array method, the expression patterns of approx. 12000 genes were analyzed, and selected genes were confirmed by a real-time quant. PCR method. The anal. of downregulated genes in the DSS mice following PPAR.gamma. administration revealed several functional gene clusters with altered expression: (1) oncogene families such as GRO1 oncogenes, (2) inflammatory mediator-related genes such as the interferon-gamma gene, (3) water electrolyte-assocd. genes, and (4) others. This is the first demonstration of global gene expression anal. using the DSS colitis mouse model with a PPAR.gamma. ligand, and these results provide new insight for finding novel target genes for treating IBD.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 103 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:947504 CAPLUS <<LOGINID::20100206>>
DN 138:54491
TI Proteomic analysis of human eosinophil activation mediated by mast cells, granulocyte macrophage colony stimulating factor and tumor necrosis factor alpha
AU Levi-Schaffer, Francesca; Temkin, Vladislav; Simon, Hans-Uwe; Kettman, John-R.; Frey, Johann-Rudolf; Lefkovits, Ivan
CS Department of Pharmacology, The Hebrew University of Jerusalem, Jerusalem, 91120, Israel
SO Proteomics (2002), 2(11), 1616-1626 CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
AB The authors assessed mast cell influence on eosinophils, the prominent cells in late and chronic allergic reactions, by comparing the proteomic pattern of eosinophils incubated with mast cells, tumor necrosis factor alpha (TNF-.alpha.) or granulocyte macrophage colony stimulating factor (GM-CSF). Eosinophils were incubated with the human mast cell line HMC-1 cellular sonicate and their survival and GM-CSF prodn. were evaluated. For proteomic studies, eosinophils were cultured with HMC-1 sonicate, TNF-.alpha. or GM-CSF in the presence of [35S]methionine, solubilized and submitted to isoelec. focusing sepn. and SDS-PAGE in the ISODALT system, followed by radio-fluorog. and computer image anal. HMC-1-incubated eosinophils displayed increased survival partly mediated by mast cell-assocd. TNF-.alpha., and produced GM-CSF. Metabolically labeled eosinophils incubated with either HMC-1, TNF-.alpha. or GM-CSF released eosinophil peroxidase. Comparison of two-dimensional gel spots from the eosinophils revealed that each of the three ***activating*** signals yielded a distinctly ***different*** ***proteomic*** pattern of labeled polypeptides. GM-CSF provided the strongest signal and the highest rate of protein synthesis (1018 spots) followed by TNF-.alpha. (747 spots) and HMC-1 sonicate (611 spots). A portion of spots differed both in terms of quality and quantity. Although each stimulus induced similar functional effects, the resulting biosynthetic programs of the eosinophils greatly differed. The presented proteomic anal. is the first step in the exploration of mol. mechanisms involved in eosinophil activation.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 104 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:928713 CAPLUS <<LOGINID::20100206>>
DN 139:32644
TI Current state of the methodology for disease proteomics
AU Kawakami, Takao; Nishimura, Toshihide
CS Research Division, GlaxoSmithKline K.K., Japan
SO Jikken Igaku (2002), 20(14), 2002-2008 CODEN: JIGEF; ISSN: 0288-5514
PB Yodosha
DT Journal; General Review
LA Japanese
AB A review on the methodologies for disease proteomics pursuing the cause for disease by analyzing the quant. ***difference*** in disease marker proteins between ***proteomes*** accompanied with the time-series of disease, ***drug*** administration or else. Examples are shown with the early diagnosis of diabetes and cancer utilizing proteomics and bioinformatics.

L12 ANSWER 105 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:915848 CAPLUS <<LOGINID::20100206>>
DN 139:94447
TI Random mutagenesis in the mouse as a tool in drug discovery
AU Russ, Andreas; Stumm, Gabriele; Augustin, Martin; Sedlmeier, Reinhard; Wattler, Sigrid; Nehls, Michael
CS Ingenium Pharmaceuticals, Martinsried, D-82152, Germany
SO Drug Discovery Today (2002), 7(23), 1175-1183 CODEN: DDTOFS; ISSN: 1359-6446
PB Elsevier Science Ltd.
DT Journal; General Review
LA English
AB A review. The flood of raw information generated by large-scale data acquisition technologies in genomics, microarrays and ***proteomics*** is ***changing*** the early stages of the ***drug*** discovery process. Although many more potential drug targets are now available compared with the pre-genomics era, knowledge about the physiol. context in which these targets act - information crucial to both discovery and development - is scarce. Random mutagenesis strategies in the mouse provide scalable approaches for both the gene-driven validation of candidate targets in vivo and the discovery of new physiol. pathways by phenotype-driven screens. Random mutagenesis strategies in the mouse provide scalable approaches for both the gene-driven validation of candidate targets in vivo and the discovery of new physiol. pathways by phenotype-driven screens.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 106 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:914712 CAPLUS <<LOGINID::20100206>>
DN 138:12045
TI cDNA clones associated with maintenance of smooth muscle cell differentiation from human and chicken, and use in drug screening and diagnosis
IN Funahashi, Shinichi; Miyata, Shoji; Sofue, Kenji; Hayashi, Kenichiro
PA Sysmex Co., Ltd., Japan; Chugai Pharmaceutical Co., Ltd.
SO Jpn. Kokai Tokkyo Koho, 75 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI JP 2002345490 A 20021203 JP 2001-343870 20011108
PRAI JP 2000-344379 A 20001110
AB cDNA clones from human and chicken coding for proteins assocd. with maintenance of smooth muscle cell differentiation, recombinant expression, antibodies, and use in screening of compds. that bind to it, are disclosed. Screened compds. can be used for treatment of diseases assocd. with abnormal proliferation of smooth muscle cells. Diagnosis of such diseases by anal. of expression of those genes is claimed. A cDNA fragment participating in the maintenance of smooth muscle differentiation was isolated from chick gizzard smooth muscle cells by differential display and the subtracted hybridization method. Gene expression profile anal. by DNA microarray revealed 79 novel genes and 13 known genes whose expression was elevated in differentiated smooth muscle cells.

L12 ANSWER 107 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:899767 CAPLUS <<LOGINID::20100206>>
DN 138:250529
TI Trifunctional chemical probes for the consolidated detection and identification of enzyme activities from complex proteomes
AU Adam, Gregory C.; Sorensen, Erik J.; Cravatt, Benjamin F.
CS The Skaggs Institute for Chemical Biology and the Department of Chemistry, The Scripps Research Institute, La Jolla, CA, 92037, USA
SO Molecular and Cellular Proteomics (2002), 1(10), 828-835 CODEN: MCPOBS; ISSN: 1535-9476
PB American Society for Biochemistry and Molecular Biology, Inc.
DT Journal
LA English
CS CASREACT 138:250529
AB Chem. probes that covalently modify the active sites of enzymes in complex proteomes are useful tools for identifying enzyme activities assocd. with discrete (patho)physiol. states. Researchers in proteomics typically use two types of activity-based probes to fulfill complementary objectives: fluorescent probes for rapid and sensitive target detection and biotinylated probes for target purifn. and identification. Accordingly, we hypothesized that a strategy in which the target detection and target isolation steps of ***activity*** -based ***proteomic*** expts. were merged might accelerate the characterization of ***differentially*** expressed protein ***activities*** . Here we report the synthesis and application of trifunctional chem. proteomic probes in which elements for both target detection (e.g. rhodamine) and isolation (e.g. biotin) are appended to a sulfonate ester reactive group, permitting the consolidated visualization and affinity purifn. of labeled proteins by a combination of in-gel fluorescence and avidin chromatog. procedures. A trifunctional Ph sulfonate probe was used to identify several tech. challenging protein targets, including the integral membrane enzyme 3.beta.-hydroxysteroid dehydrogenase/.DELTA.5-isomerase and the cofactor-dependent enzymes platelet-type phosphofructokinase and type II tissue transglutaminase. The latter two enzyme activities were significantly up-regulated in the invasive estrogen receptor-neg. (ER-)) human breast cancer cell line MDA-MB-231 relative to the non-invasive ER+) breast cancer lines MCF7 and T-47D. Collectively these studies demonstrate that chem. proteomic probes incorporating elements for both target detection and target isolation fortify the important link between the visualization of differentially expressed enzyme activities and their subsequent mol. identification, thereby augmenting the information content achieved in activity-based profiling expts.
OSC.G 55 THERE ARE 55 CAPLUS RECORDS THAT CITE THIS RECORD (55 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 108 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:892142 CAPLUS <<LOGINID::20100206>>
DN 138:184924
TI Functional proteomics to study protection of the ischaemic myocardium
AU Vondriska, Thomas M.; Ping, Peipei
CS Departments of Physiology and Medicine/Division of Cardiology, University of California, Los Angeles, CA, 90095, USA
SO Expert Opinion on Therapeutic Targets (2002), 6(5), 563-570 CODEN: EOTTAO; ISSN: 1472-8222
PB Ashley Publications Ltd.
DT Journal; General Review
LA English
AB A review. Mechanisms to reduce the deleterious effects of myocardial ischemia are of particular clin. importance and were the focus of intense research for a no. of years. Among novel approaches to studying the ischemic heart, proteomics, or the anal. of all cellular proteins, presents as a powerful method to deconstruct the mechanisms of disease and protection. Specifically, the field of functional proteomics is an emerging application of proteomics that melds aspects of classical proteomics, biochem., mol. biol. and physiol. into an approach that facilitates an understanding of how proteins and protein interactions engender phenotype. This review highlights ***different*** types of proteomic applications and provides a prospectus for functional ***proteomics*** as a robust vehicle driving ***drug*** discovery and design.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 109 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:863744 CAPLUS <<LOGINID::20100206>>
DN 138:88445
TI Expression profile of leukocyte genes activated by anti-neutrophil cytoplasmic autoantibodies (ANCA)
AU Yang, Jia Jin; Preston, Gloria A.; Alcorta, David A.; Waga, Iwao; Munger, William E.; Hogan, Susan L.; Sekura, Stephen B.; Phillips, Brian D.; Thomas, Robin P.; Jennette, J. Charles; Falk, Ronald J.

CS Division of Nephrology, Department of Medicine, The University of North Carolina, Chapel Hill, NC, USA
SO Kidney International (2002), 62(5), 1638-1649 CODEN: KDYIA5; ISSN: 0085-2538
PB Blackwell Publishing, Inc.
DT Journal
LA English
AB Background. Anti-neutrophil cytoplasmic autoantibodies (ANCA) induce neutrophil activation in vitro with release of injurious products that can mediate necrotizing vasculitis in vivo. The importance of ANCA IgG F(ab')2-antigen binding vs. Fc.gamma. receptor engagement in this process is controversial. We propose that ANCA-antigen binding affects cell signaling pathways that can result in changes of gene expression. Methods. Microarray GeneChip anal. and real-time, quant. PCR (TaqMan) was used to probe for transcripts in leukocytes from patients (in vivo gene expression study) and in leukocytes treated with ANCA IgG or ANCA-F(ab')2 (in vitro gene expression study). Results. Microarray gene chip anal. showed that ANCA IgG and ANCA-F(ab')2 stimulate transcription of a distinct subset of genes, some unique to whole IgG, some unique to F(ab')2 fragments, and some common to both. DIF-2, COX-2, and IL-8 were identified as genes responsive to ANCA signaling and were selected for in depth evaluation. In vitro DIF-2 and IL-8 were increased by both ANCA IgG and F(ab')2, but COX-2 only by MPO-ANCA F(ab')2. In vivo DIF-2 levels were increased in leukocytes of ANCA patients, which correlated strongly with disease activity and ANCA titer. DIF-2 was not increased in patients in remission or in disease control patients (systemic lupus erythematosus and IgA nephropathy). COX-2 gene expression was significantly increased in patients with active disease, while IL-8 was increased in remission. Conclusions. The data indicate that leukocyte genes are activated in vitro by both ANCA Fe and ANCA F(ab')2 pathways and that in vitro activation mimics changes in circulating leukocytes of patients with ANCA disease. Increased levels of DIF-2 in patient leukocytes strongly correlate with severity of disease in kidney tissue. The observations indicate a previously unrecognized role for DIF-2 in ANCA-mediated inflammation, which raises the possibility that DIF-2 has an important role in other types of inflammation.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 110 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:859003 CAPLUS <<LOGINID::20100206>>
DN 138:135723
TI A molecular analysis of ascidian metamorphosis reveals activation of an innate immune response
AU Davidson, Brad; Swalla, Billie J.
CS Zoology Department and Center for Developmental Biology, University of Washington, Seattle, WA, 98195-1800, USA
SO Development (Cambridge, United Kingdom) (2002), 129(20), 4739-4751 CODEN: DEVPED; ISSN: 0950-1991
PB Company of Biologists Ltd.
DT Journal
LA English
AB Ascidian metamorphosis represents a powerful model for comparative work on chordate development that has remained largely unexplored. We isolated transcripts differentially expressed during metamorphosis in the ascidian Boltenia villosa by suppressive PCR subtractions of staged larval and juvenile cDNAs. We employed a series of three subtractions to dissect gene expression during metamorphosis. We have isolated 132 different protein coding sequences, and 65 of these transcripts show significant matches to GenBank proteins. Some of these genes have putative functions relevant to key metamorphic events including the differentiation of smooth muscle, blood cells, heart tissue and adult nervous system from larval rudiments. In addn., a significant fraction of the differentially expressed transcripts match identified genes from the innate immune system. Innate immunity confers a rapid response to pathogen-specific mols. and/or compromised self-tissues. The activation of innate immunity genes during metamorphosis may represent the programmed maturation of the adult immune system. In addn., this immune response may be necessary for phagocytosis and re-structuring of larval tissues. An innate immune-related inflammatory response may also underlie two waves of trans-epidermal blood cell migration that occur during the swimming larval period and immediately upon settlement. We characterized these trans-epidermal migrations and discovered that some migratory cells leave the animal entirely through an anterior tunnel in the tunic. We show that these cells are positioned to detect external settlement cues and hypothesize that the innate immune system may also be employed to detect and rapidly respond to environmental settlement cues.
OSC.G 32 THERE ARE 32 CAPLUS RECORDS THAT CITE THIS RECORD (32 CITINGS)
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 111 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:843847 CAPLUS <<LOGINID::20100206>>
DN 138:148587
TI A fast fiber enhancer exists in the muscle regulatory factor 4 gene promoter
AU Pin, Christopher L.; Konieczny, Stephen F.
CS Departments of Paediatrics and Physiology and Pharmacology, University of Western Ontario, Child Health Research Institute, London, ON, N6C 2V5, Can.
SO Biochemical and Biophysical Research Communications (2002), 299(1), 7-13 CODEN: BBRCA9; ISSN: 0006-291X
PB Elsevier Science
DT Journal
LA English
AB The development of skeletal muscle is a highly regulated process governed by the four myogenic regulatory factors (MRFs) MyoD, myf-5, myogenin, and MRF4. While these factors exhibit some unique functions, part of their individual ***activity*** can be attributed to ***different*** temporal and spatial ***expression*** ***patterns*** . To delineate the factors that control expression of the MRFs, the authors have begun a mol. dissection of the MRF4 gene promoter. Through the generation of promoter/reporter gene constructs, the authors show that an 853 bp fragment, residing 4 kb upstream of the MRF4 transcriptional start site (853AV), is able to enhance expression of the basal MRF4 promoter 3-4-fold in myogenic cell cultures. Anal. of the 853AV enhancer in transgenic mice indicates that this region drives MRF4 gene expression primarily in fast muscle fibers, suggesting that the normal adult MRF4 expression pattern is regulated by a variety of control elements that may dictate fiber-type specificity.
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 112 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:833386 CAPLUS <<LOGINID::20100206>>
DN 137:334080
TI Genes differentially expressed in human colon cancer and their diagnostic and therapeutic uses
IN Lasek, Amy W.; Jones, David A.
PA USA
SO U.S. Pat. Appl. Publ., 231 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 20020160382 A1 20021031 US 2001-981353 20011011
PRAI US 2000-239841P P 20001011
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The present invention relates to a combination comprising a plurality of cDNAs which are differentially expressed in colon cancer, or in a precancerous condition of the colon. Differential expression was detected using the HUMAN GENOME GEM series 1-3 microarrays (Incyte Genomics) contg. 28,626 array elements, which represent 10,068 annotated clusters and 18,558 unannotated clusters. Array elements that exhibited .gtoreq.2-fold change in expression, a signal intensity over 250 units, a signal-to-background ratio of at least 2.5, and an element spot size of .gtoreq.40% were identified as differentially expressed. These genes are useful as diagnostic markers or as potential therapeutic targets for premalignant colon polyps or colon cancer. These marker genes and proteins may be used in their entirety or in part as to diagnose, stage, treat, or monitor the treatment of a subject with a colon cancer.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L12 ANSWER 113 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:832556 CAPLUS <<LOGINID::20100206>>
DN 137:350862
TI Gene expression profiles in bone and cartilage formation and their use in diagnosis and treatment of disease
IN Clancy, Brian; Pittman, Debra M.
PA Wyeth, John, and Brother Ltd., USA
SO PCT Int. Appl., 197 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002085285 A2 20021031 WO 2002-US12149 20020418
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-284786P P 20010418
AB The invention provides methods and comps. for diagnostic assays for detecting bone and cartilage formation and therapeutic methods and comps. for treating disease and disorders related to bone and cartilage formation or resorption, such as osteoporosis and bone fractions. The invention also provides therapeutic methods for diseases related to bone or cartilage formation or resorption. Methods for identifying therapeutics for such diseases are also provided. Marker genes that can be used to monitor bone and cartilage formation are identified on com. DNA microarrays.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 114 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:818032 CAPLUS <<LOGINID::20100206>>
DN 138:85479
TI Isolation, cloning and expression of a multifunctional O-methyltransferase capable of forming 2,5-dimethyl-4-methoxy-3(2H)-furanone, one of the key aroma compounds in strawberry fruits
AU Wein, Martina; Lavid, Noa; Lunkenbein, Stefan; Lewinsohn, Efraim; Schwab, Wilfried; Kaldenhoff, Ralf
CS Lehrstuhl fuer Lebensmittelchemie, Universitaet Wuerzburg, Wuerzburg, 97074, Germany
SO Plant Journal (2002), 31(6), 755-765 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB Strawberry fruits contain an uncommon group of key aroma compds. with a 2,5-dimethyl-3(2H)-furanone structure. Here, we report on the methylation of 2,5-dimethyl-4-hydroxy-3(2H)-furanone (DMHF) to 2,5-dimethyl-4-methoxy-3(2H)-furanone (DMMF) by a S-adenosyl-L-methionine dependent O-methyltransferase, the cloning of the corresponding cDNA and characterization of the encoded protein. Northern-hybridization indicated that the Strawberry-OMT specific transcripts accumulated during ripening in strawberry fruits and were absent in root, petiole, leaf and flower. The protein was functionally expressed in E. coli and exhibited a substrate specificity for catechol, caffeic acid, protocatechuic aldehyde, caffeoyl CoA and DMHF. A common structural feature of the accepted substrates was a o-diphenolic structure also present in DMHF in its dienolic tautomer. FaOMT is active as a homodimer and the native enzyme shows optimum activity at pH 8.5 and 37.degree.. It does not require a cofactor for enzymic activity. Due to the ***expression*** ***pattern*** of FaOMT and the enzymic ***activity*** in the ***different*** stages of fruit ripening we suppose that FaOMT is involved in lignification of the achenes and the vascular bundles in the expanding fruit. In addn., it is concluded that the Strawberry-OMT plays an important role in the biosynthesis of strawberry volatiles such as vanillin and DMMF.
OSC.G 41 THERE ARE 41 CAPLUS RECORDS THAT CITE THIS RECORD (41 CITINGS)
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 115 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:811882 CAPLUS <<LOGINID::20100206>>
DN 138:219138

TI Differential gene expression profiles of gastric cancer cells established from primary tumor and malignant ascites
AU Sakakura, C.; Hagiwara, A.; Nakanishi, M.; Shimomura, K.; Takagi, T.; Yasuoka, R.; Fujita, Y.; Abe, T.; Ichikawa, Y.; Takahashi, S.; Ishikawa, T.; Nishizuka, I.; Morita, T.; Shimada, H.; Okazaki, Y.; Hayashizaki, Y.; Yamagishi, H.
CS Department of Digestive Surgery, Kyoto Prefectural University of Medicine, Kawaramachi-dori, Kyoto, Kamigyo-ku, 602-8566, Japan
SO British Journal of Cancer (2002), 87(10), 1153-1161 CODEN: BJCAAI; ISSN: 0007-0920
PB Nature Publishing Group
DT Journal
LA English
AB Advanced gastric cancer is often accompanied by metastasis to the peritoneum, resulting in a high mortality rate. Mechanisms involved in gastric cancer metastasis have not been fully clarified because metastasis involves multiple steps and requires a combination of altered expressions of many different genes. Thus, independent anal. of any single gene would be insufficient to understand all of the aspects of gastric cancer peritoneal dissemination. In this study, we performed a global anal. of the differential gene expression of a gastric cancer cell line established from a primary main tumor (SNU-1) and of other cell lines established from the metastasis to the peritoneal cavity (SNU-5, SNU-16, SNU-620, KATO-III and GT3TKB). The application of a high-d. cDNA microarray method made it possible to analyze the expression of approx. 21 168 genes. Our examns. of SNU-5, SNU-16, SNU-620, KATO-III and GT3TKB showed that 24 genes were up-regulated and 17 genes down-regulated besides expression sequence tags. The anal. revealed the following altered expression such as: (a) up-regulation of CD44 (cell adhesion), keratins 7, 8, and 14 (epithelial marker), aldehyde dehydrogenase (drug metab.), CD9 and IP3 receptor type 3 (signal transduction); (b) down-regulation of IL2 receptor .gamma., IL4-Stat (immune response), p27 (cell cycle) and integrin .beta.4 (adhesion) in gastric cancer cells from malignant ascites. We then analyzed eight gastric cancer cell lines with Northern blot and obsd. preferential up-regulation and down-regulation of these selected genes in cells prone to peritoneal dissemination. Reverse transcriptase-polymerase chain reaction confirmed that several genes selected by DNA microarray were also overexpressed in clin. samples of malignant ascites. It is therefore considered that these genes may be related to the peritoneal dissemination of gastric cancers. The results of this global gene expression anal. of gastric cancer cells with peritoneal dissemination, promise to provide a new insight into the study of human gastric cancer peritoneal dissemination.
OSC.G 46 THERE ARE 46 CAPLUS RECORDS THAT CITE THIS RECORD (46 CITINGS)
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 116 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:795276 CAPLUS <<LOGINID::20100206>>
DN 138:218588
TI A molecular profile of a hematopoietic stem cell niche
AU Hackney, Jason A.; Charbord, Pierre; Brunk, Brian P.; Stoeckert, Christian J.; Lemischka, Ihor R.; Moore, Kateri A.
CS Department of Molecular Biology, Princeton University, Princeton, NJ, 08544, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(20), 13061-13066 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The hematopoietic microenvironment provides a complex mol. milieu that regulates the self-renewal and differentiation activities of stem cells. A stem cell supportive stromal cell line, AFT024, that was derived from murine fetal liver, has been characterized. Highly purified in vivo transplantable mouse stem cells are maintained in AFT024 cultures at input levels, whereas other primitive progenitors are expanded. In addn., human stem cells are very effectively supported by AFT024. The AFT024 cell line may represent a component of an in vivo stem cell niche. To det. the mol. signals elaborated in this niche, a functional genomics approach was undertaken that combines extensive sequence mining of a subtracted cDNA library, high-d. array hybridization, and in-depth bioinformatic analyses. The data were assembled into a biol. process oriented database, and represent a mol. profile of a candidate stem cell niche. A total of 5975 expressed sequence tag (EST) sequences are deposited in GenBank/EMBL/DDBJ under accession nos. BQ827747-BQ833721.
OSC.G 91 THERE ARE 91 CAPLUS RECORDS THAT CITE THIS RECORD (92 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 117 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:783185 CAPLUS <<LOGINID::20100206>>
DN 138:68063
TI The Yeast Iron Regulon Is Induced upon Cobalt Stress and Crucial for Cobalt Tolerance
AU Stadler, Jochen A.; Schweyen, Rudolf J.
CS Institute of Microbiology and Genetics, Vienna Biocenter, University of Vienna, Vienna, A-1030, Austria
SO Journal of Biological Chemistry (2002), 277(42), 39649-39654 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB To identify yeast genes involved in cobalt detoxification, we performed RNA ***expression*** ***profiling*** expts. and followed ***changes*** in gene ***activity*** upon cobalt stress on a genome-wide scale. We found that cobalt stress specifically results in an immediate and dramatic induction of genes involved in iron uptake. This response is dependent on the Aft1 protein, a transcriptional factor known to regulate a set of genes involved in iron uptake and homeostasis (iron regulon). Like iron starvation, cobalt stress induces accumulation of the Aft1 protein in the nucleus to activate transcription of its target genes. Cells lacking the AFT1 gene (aft1) are hypersensitive to cobalt as well as to other transition metals, whereas expression of the dominant AFT1-1up allele, which results in up-regulation of AFT1-controlled genes, confers resistance. Cobalt resistance correlates with an increase in intracellular iron in AFT1-1up cells, and sensitivity of aft1 cells is assocd. with a lack of iron accumulation. Furthermore, elevated iron levels in the growth medium suppress the cobalt sensitivity of the aft1 mutant cells, even though they increase cellular cobalt. Results presented indicate that yeast cells acquire cobalt tolerance by activating the Aft1p-dependent iron regulon and thereby increasing intracellular iron levels.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)

RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 118 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:778194 CAPLUS <<LOGINID::20100206>>
DN 137:274046
TI Screening renal-generative agents using differential gene expression profile DNA microarray analysis
IN Peyman, John A.; Lehtonen, Eero; Crasta, Oswald R.; Cates, Richard L.
PA Quragen Corporation, USA; Biogen, Inc.
SO PCT Int. Appl., 30 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002079489 A2 20021010 WO 2002-US10017 20020401
WO 2002079489 A3 20031120
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
AU 2002252560 A1 20021015 AU 2002-252560 20020401
US 20030073100 A1 20030417 US 2002-113312 20020401
PRAI US 2001-280258P P 20010330
WO 2002-US10017 W 20020401
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB Disclosed are methods of identifying renal-generative agents using differential gene expression. Also disclosed are methods of treating renal disorders. The present invention is based in part on the discovery of changes in expression patterns of multiple nucleic acid sequences in murine metanephric mesenchyme undergoing mesenchymal-epithelial transition (MET). The differentially expressed nucleic acids were identified by inducing epithialization of murine metanephric mesenchyme explants. Genes whose transcript levels varied relative to the control samples were identified using GENECALLINGTM differential expression anal. as described in U.S. Patent No. 5,871,697 and in Shimkets and al., Nature Biotechnol. 17:798-803 (1999). Two hundred and forty five genes were found to be differentially expressed in epithelialized metanephric mesenchyme. These sequences are referred to herein as MET 1-261 A summary of the MET sequences analyzed is presented in Tables 1 and 2 One hundred and forty eight genes were upregulated as shown in Table 1. Ninety seven genes were downregulated as shown in Table 2.

L12 ANSWER 119 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:777054 CAPLUS <<LOGINID::20100206>>
DN 138:364885
TI Proteome analysis of the activation of rat hepatic stellate cells
AU Yamagata, Akira; Yoshizato, Katsutoshi
CS Biotechnology Research Lab., Towa Science Co., Ltd., Japan
SO Igaku no Ayumi (2002), 202(5), 347-352 CODEN: IGAYAY; ISSN: 0039-2359
PB Ishiyaku Shuppan
DT Journal; General Review
LA Japanese
AB A review. General approach in proteome anal. by 2D electrophoresis was first described. The recent findings on gene expression profiles of hepatic stellate cells of the activated status were summarized. The ***difference*** in ***expression** ***profiles*** between in vitro and in vivo ***activation*** , function of newly identified protein such as STAP, and the relationship of stellate cell activation to reconstitution of extracellular matrix proteins were discussed. The potential application of the findings obtained by the proteome analyses to the screening of drugs for liver fibrosis was also discussed.

L12 ANSWER 120 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:776961 CAPLUS <<LOGINID::20100206>>
DN 138:364884
TI Apoptosis and proteomics
AU Kuramitsu, Yasuhiro; Nakamura, Kazuyuki
CS School of Medicine, Yamaguchi University, Japan
SO Igaku no Ayumi (2002), 202(5), 343-346 CODEN: IGAYAY; ISSN: 0039-2359
PB Ishiyaku Shuppan
DT Journal; General Review
LA Japanese
AB A review gives an overview on proteomic anal. of apoptotic cells by using 2D-gel electrophoresis. The proteins identified as apoptosis-assocd. factors were summarized. These proteins included cytokeratin 18, peroxiredoxin 4, caspases -3 and -4, cathepsin D, hsp27, STAT3, Bcl-2, p-STAT3, stathmin, thymosin .beta.-4, and eif-5A. Some specific proteins were described regarding how they were identified as apoptosis-assocd. factors during heat treatment or TNF-.alpha. treatment that induced apoptosis. ***Proteomic*** comparison of liver cancer cells with ***different*** sensitivity to anti-cancer ***drug*** that lead to the identification phosphatidylethanolamine-binding protein as apoptosis-repressing protein was also presented with actual 2D electrophoresis results.

L12 ANSWER 121 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:773332 CAPLUS <<LOGINID::20100206>>
DN 138:19598
TI The structure and function of vertebrate fibroblast growth factor receptor 1
AU Groth, Casper; Lardelli, Michael
CS Department of Molecular Biosciences and Special Research Centre for the Molecular Genetics of Development, Adelaide University, Adelaide, Australia
SO International Journal of Developmental Biology (2002), 46(4, Spec.), 393-400 CODEN: IJDBE5; ISSN: 0214-6282
PB University of the Basque Country Press
DT Journal; General Review
LA English
AB A review. The vertebrate fibroblast growth factor receptor 1 (FGFR1) is alternatively spliced generating multiple splice variants that are differentially expressed during embryo development and in the adult body. The restricted ***expression*** ***patterns*** of FGFR1 isoforms, together with ***differential*** expression and binding of specific ligands, leads to ***activation*** of common FGFR1 signal transduction pathways, but may result in distinctively different

biol. responses as a result of differences in cellular context. FGFR1 isoforms are also present in the nucleus in complex with various fibroblast growth factors where they function to regulate transcription of target genes.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)
RE.CNT 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 122 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:750326 CAPLUS <<LOGINID::20100206>>
DN 138:348521
TI Comparison of Human Duodenum and Caco-2 Gene Expression Profiles for 12,000 Gene Sequences Tags and Correlation with Permeability of 26 Drugs
AU Sun, Duxin; Lennernas, Hans; Welage, Lynda S.; Barnett, Jeffery L.; Landowski, Christopher P.; Foster, David; Fleisher, David; Lee, Kyung-Dall; Amidon, Gordon L.
CS Department of Pharmaceutical Sciences, College of Pharmacy, University of Michigan, Ann Arbor, MI, 48109, USA
SO Pharmaceutical Research (2002), 19(10), 1400-1416
CODEN: PHREEB; ISSN: 0724-8741
PB Kluwer Academic/Plenum Publishers
DT Journal
LA English
AB To compare gene ***expression*** ***profiles*** and ***drug*** permeability ***differences*** in Caco-2 cell culture and human duodenum. Gene expression profiles in Caco-2 cells and human duodenum were detd. by GeneChip anal. In vivo drug permeability measurements were obtained through single-pass intestinal perfusion in human subjects, and correlated with in vitro Caco-2 transport permeability. GeneChip anal. detd. that 37, 47, and 44 % of the 12,559 gene sequences were expressed in 4-day and16-day Caco-2 cells and human duodenum, resp. Comparing human duodenum with Caco-2 cells, more than 1000 sequences were detd. to have at least a 5-fold difference in expression. There were 26, 38, and 44 % of the 443 transporters, channels, and metabolizing enzymes detected in 4-day, 16-day Caco-2 cells, and human duodenum, resp. More than 70 transporters and metabolizing enzymes exhibited at least a 3-fold difference. The overall coeff. of variability of the 10 human duodenal samples for all expressed sequences was 31% (range 3% to 294%) while that of the expressed transporters and metabolizing enzymes was 33% (range 3% to 87%). The in vivo / in vitro drug permeability measurements correlated well for passively absorbed drugs (R2 = 85%). The permeability correlation for carrier-mediated drugs showed 3- 35-fold higher in human above the correlation of passively absorbed drugs. The 2- 595-fold differences in gene expression levels between the Caco-2 cells and human duodenum correlated with the obsd. 3- 35-fold difference in permeability correlation between carrier-mediated drugs and passively absorbed drugs. Significant differences in gene expression levels in Caco-2 cells and human duodenum were obsd. The obsd. differences of gene expression levels were consistent with obsd. differences in carrier mediated drug permeabilities. Gene expression profiling is a valuable new tool for investigating in vitro and in vivo permeability correlation.
OSC.G 101 THERE ARE 101 CAPLUS RECORDS THAT CITE THIS RECORD (101 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 123 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:728286 CAPLUS <<LOGINID::20100206>>
DN 138:101704
TI Cloning and characterization of the expression pattern of a novel splice product MIA (splice) of malignant melanoma-derived growth-inhibiting activity (MIA/CD-RAP)
AU Hau, Peter; Wise, Petra; Bosserhoff, Anja-Katrin; Blesch, Armin; Jachimczak, Piotr; Tschertner, Ines; Bogdahn, Ulrich; Apfel, Rainer
CS Department of Neurology, University of Regensburg, Regensburg, 93053, Germany
SO Journal of Investigative Dermatology (2002), 119(3), 562-569 CODEN: JIDEAE; ISSN: 0022-202X
PB Blackwell Publishing, Inc.
DT Journal
LA English
AB Melanoma-inhibiting activity/cartilage-derived retinoic acid-sensitive protein, a 11 kDa protein, is mainly expressed in cartilage during embryogenesis, and is related to invasion, metastasis, and immuno-modulation of melanoma and glioma cells in vivo and in vitro. Here, we describe an alternative splice product of this gene termed melanoma-inhibiting activity (splice), lacking exon 2 of the original protein. A predicted frameshift by alternate splicing results in a unique C-terminal portion of the protein. Consistent with this, a protein migrating at the predicted mol. wt. of the splice form (3.5 kDa) was detected using an N-terminal specific antibody. This band was undetectable when using a C-terminal specific antibody. In addn., we describe the ***expression*** ***pattern*** of melanoma-inhibiting ***activity*** (splice) in ***different*** human tumors. Expression was shown in tissue samples of five of six primary melanomas, 11 of 12 primary sites of metastatic melanomas, 10 of 10 systemic metastases of melanomas, four of four central nervous system metastases of melanomas, six of eight primary melanoma cultures, and five of five melanoma cell lines. Only a faint signal was obtained in tissue samples of five of six nevi. Interestingly, seven of eight nonmelanocytic tissue samples and five of seven glioma cell lines showed weak expression of melanoma-inhibiting activity (splice). Approaching first functional aspects, reverse transcriptase-polymerase chain reaction showed weak expression of melanoma-inhibiting activity (splice) in relation to melanoma-inhibiting activity in nonmelanocytic and strong expression in melanocytic cells. Staining with a specific anti-serum raised against a synthetic peptide resembling the amino acid sequence of melanoma-inhibiting activity (splice) showed a more nuclear staining pattern in comparison with melanoma-inhibiting activity. Furthermore, incubation of melanoma and glioma cell cultures with transforming growth factor-.beta.2 showed inverse regulation of the mRNA of melanoma-inhibiting activity and melanoma-inhibiting activity (splice), both suggesting also a different function within the physiol. role of this unique family of proteins. Melanoma-inhibiting activity (splice) has no homol. to any other known protein so far. Whereas the biol. function of melanoma-inhibiting activity (splice) is not clear yet, it might provide a relevant diagnostic and therapeutic tool for malignant melanomas.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 124 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:649643 CAPLUS <<LOGINID::20100206>>

DN 138:118326
TI Identification and characterization of rapidly dividing U937 clones with ***differential*** telomerase ***activity*** and gene ***expression*** ***profiles*** : Role of c-Myc/Mad1 and Id/Ets proteins
AU Xiao, X.; Phogat, S. K.; Sidorov, I. A.; Yang, J.; Horikawa, I.; Prieto, D.; Adelesberger, J.; Lempicki, R.; Barrett, J. C.; Dimitrov, D. S.
CS NIH, Laboratory of Experimental and Computational Biology, National Cancer Institute at Frederick, Frederick, MD, USA
SO Leukemia (2002), 16(9), 1877-1880 CODEN: LEUKEI; ISSN: 0887-6924
PB Nature Publishing Group
DT Journal
LA English
AB There is a striking difference between plus and minus U937 clones in their telomerase activity, telomere length, apoptosis, growth rate and gene expression. However, they have similarity in the rate of their division as measured by BrdU incorporation. These observations suggest a possible mechanism for differential regulation of telomerase activity and cell division in these cells, a potential role for Ets1 and Ets2 in telomerase activity regulation, and the existence of another yet to be identified pathways of Id2 and telomerase regulation, which is currently under investigation. The identification of U937 clones with strikingly different telomerase activity, and differential expression of Id and Ets family proteins but similar division rates provided a unique model system to study regulation of telomerase, and other differentiation and cancer-related genes.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 125 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:649061 CAPLUS <<LOGINID::20100206>>
DN 137:322182
TI A proteomics approach for the identification of DNA binding activities observed in the electrophoretic mobility shift assay
AU Woo, Andrew J.; Dods, James S.; Susanto, Evelyn; Ulgiati, Daniela; Abraham, Lawrence J.
CS Biochemistry and Molecular Biology, School of Biomedical and Chemical Sciences and Western Australian Institute for Medical Research, The University of Western Australia, Crawley, 6009, Australia
SO Molecular and Cellular Proteomics (2002), 1(6), 472-478 CODEN: MCPOBS; ISSN: 1535-9476
PB American Society for Biochemistry and Molecular Biology, Inc.
DT Journal
LA English
AB Transcription factors lie at the center of gene regulation, and their identification is crucial to the understanding of transcription and gene expression. Traditionally, the isolation and identification of transcription factors has been a long and laborious task. We present here a novel method for the identification of DNA-binding proteins seen in electrophoretic mobility shift assay (EMSA) using the power of two-dimensional electrophoresis coupled with mass spectrometry. By coupling SDS-PAGE and isoelec. focusing to EMSA, the mol. mass and pI of a protein complex seen in EMSA were estd. Candidate proteins were then identified on a two-dimensional array at the predetd. pI and mol. mass coordinates and identified by mass spectrometry. We show here the successful isolation of a functionally relevant transcription factor and validate the identity through EMSA supershift anal.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 126 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:641311 CAPLUS <<LOGINID::20100206>>
DN 138:102279
TI Expression profiling identifies strain-specific changes associated with ethanol withdrawal in mice
AU Daniels, G. M.; Buck, K. J.
CS Department of Behavioral Neuroscience, Portland Alcohol Research Center, Portland Department of Veterans Affairs Medical Center, Oregon Health Sciences University, Portland, OR, USA
SO Genes, Brain and Behavior (2002), 1(1), 35-45 CODEN: GBBEAC; ISSN: 1601-1848
PB Blackwell Munksgaard
DT Journal
LA English
AB Mice that exhibit characteristics of phys. dependence following ethanol exposure serve as useful models of alcoholism in humans. The DBA/2J and C57BL/6J inbred strains differ in their behavioral response to ethanol withdrawal. Alterations in gene expression are believed to underlie neuroadaptation to ethanol dependence and tolerance. Therefore, the differences in ethanol withdrawal severity obsd. between the DBA/2J and C57BL/6J strains may be related to differential regulation of gene expression. We have used cDNA microarrays to det. the gene expression profile in the hippocampus of DBA/2J and C57BL/6J mice during withdrawal after chronic and acute ethanol exposure. Of the 7634 genes surveyed, approx. 2% were consistently differentially expressed by at least 1.4-fold in DBA/2J mice during chronic ethanol withdrawal. Less than 1% of the genes showed altered expression in C57BL/6J mice under the same conditions, or in DBA/2J mice during acute ethanol withdrawal. Strain- and treatment-specific patterns of altered expression were obsd. for multiple genes assocd. with the Janus kinase/signal transducers and activators of transcription and the mitogen activated protein kinase pathways. Genes assocd. with both pathways are regulated in DBA/2J mice during chronic ethanol withdrawal, and to a lesser extent during acute ethanol withdrawal. Only those genes assocd. with the mitogen-activated protein kinase (MAPK) pathway exhibited changes in expression in C57BL/6J mice during ethanol withdrawal. Furthermore, genes assocd. with retinoic acid-mediated signaling show differential expression exclusively in C57BL/6J mice. These findings represent significant differences in cellular adaptation to ethanol between the DBA/2J and C57BL/6J strains.
OSC.G 32 THERE ARE 32 CAPLUS RECORDS THAT CITE THIS RECORD (32 CITINGS)
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 127 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:639874 CAPLUS <<LOGINID::20100206>>
TI Functional cloning, sorting, and expression profiling of nucleic acid-binding proteins
AU Ramanathan, Y.; Zhang, Haibo; Aris, Virginie; Soteropoulos, Patricia; Aaronson, Stuart A.; Tolias, Peter P.

CS Center for Applied Genomics, Public Health Research Institute, International Center for Public Health W420M, Newark, NJ, 07103, USA
SO Genome Research (2002), 12(8), 1175-1184 CODEN: GERES; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal; Letter
LA English
AB A major challenge in the post-sequencing era is to elucidate the activity and biol. function of genes that reside in the human genome. An important subset includes genes that encode proteins that regulate gene expression or maintain the structural integrity of the genome. Using a novel oligonucleotide-binding substrate as bait, we show the feasibility of a modified functional expression-cloning strategy to identify human cDNAs that encode a spectrum of nucleic acid-binding proteins (NBPs). Approx. 170 cDNAs were identified from screening phage libraries derived from a human colorectal adenocarcinoma cell line and from noncancerous fetal lung tissue. Sequence anal. confirmed that virtually every clone contained a known DNA- or RNA-binding motif. We also report on a complementary sorting strategy that, in the absence of subcloning and protein purifn., can distinguish different classes of NBPs according to their particular binding properties. To extend our functional annotation of NBPs, we have used GeneChip ***expression*** ***profiling*** of 14 ***different*** breast-derived cell lines to examine the relative transcriptional ***activity*** of genes identified in our screen and cluster anal. to discover other genes that have similar expression patterns. Finally, we present strategies to analyze the upstream regulatory region of each gene within a cluster group and select unique combinations of transcription factor binding sites that may be responsible for dictating the obsd. synexpression.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 128 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:614179 CAPLUS <<LOGINID::20100206>>
TI 3-D cell culture effects on cell cycle: Productivity and proteome of CHO cells
AU Luo, Jun; Yang, Shang-Tian
CS Department of Chemical engineering, Ohio State University, Columbus, OH, 43210, USA
SO Abstracts of Papers, 224th ACS National Meeting, Boston, MA, United States, August 18-22, 2002 (2002), BIOT-223 Publisher: American Chemical Society, Washington, D. C. CODEN: 69CZPZ
DT Conference; Meeting Abstract
LA English
AB Cells cultured in three-dimensional (3D) environment showed different physiol. and biochem. characteristics in their proliferation and differentiation compared with cells grown on 2D surfaces. The growth behavior and productivity of the Chinese hamster ovary (CHO) cell line, engineered to synthesize the secreted alk. phosphatase (SEAP), were characterized in 2D and 3D environments. A 3D cultivation provided 1.5-fold increase of specific productivity. More significant effects were obtained during long-term cultures. Sepn. of total protein exts. by two-dimensional gel electrophoresis showed altered expression levels of CHO proteins for cells transferred from 2D to 3D environment. These ***changes*** in the ***proteome*** suggest that mammalian cells respond ***actively*** to ***different*** culture environments by synthesizing specific environment-inducible proteins. This provides better understand the environmental effects on cell culturing and further improves the bioreactor design and cell culture process.

L12 ANSWER 129 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:613967 CAPLUS <<LOGINID::20100206>>
TI Isoelectric focusing-based multidimensional separation platforms with nano-ESI-MS/MS for proteomic studies of steroid-induced programmed cell death during development
AU Chen, Jinzhi; Mohan, Deepa; Balgley, Brian M.; Baehrecke, Eric H.; Shen, Yufeng; Smith, Richard D.; Lee, Cheng S.
CS Department of Chemistry and Biochemistry, University of Maryland, College Park, MD, 20742, USA
SO Abstracts of Papers, 224th ACS National Meeting, Boston, MA, United States, August 18-22, 2002 (2002), BIOT-010 Publisher: American Chemical Society, Washington, D. C. CODEN: 69CZPZ
DT Conference; Meeting Abstract
LA English
AB This project represents an integrated research effort combining the development of two isoelec. focusing-based multidimensional sepn. platforms for proteome anal., application of these technologies to studies of protein expression relating to cell death, incorporation of the resulting protein expression data with novel bioinformatics tools, and utilization of these tools for the characterization of ***changes*** in the transcriptome and ***proteome*** during steroid ***activation*** of programmed cell death. Ultrahigh resolving power together with significant enhancement in analyte concn. contributed by these multidimensional sepn. platforms are demonstrated, particularly for the anal. of low abundant proteins involved in steroid-triggered programmed cell death in Drosophila. By combining the strength of our proteome technologies with the knowledge in Drosophila genetics, the results gathered in this study provide valuable information toward the difference between autophagy and apoptosis and the novel protein signaling pathways that mediate steroid-triggered cell death.

L12 ANSWER 130 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:593693 CAPLUS <<LOGINID::20100206>>
DN 138:147311
TI Gene expression profiles with activation of the estrogen receptor .alpha.-selective estrogen receptor modulator complex in breast cancer cells expressing wild-type estrogen receptor
AU Levenson, Anait S.; Svoboda, Kristen M.; Pease, Katherine M.; Kaiser, Scott A.; Chen, Bin; Simons, Laura A.; Jovanovic, Borko D.; Dyck, Patricia A.; Jordan, V. Craig
CS Robert H. Lurie Comprehensive Cancer Center, The Feinberg School of Medicine, Northwestern University, Chicago, IL, 60611, USA
SO Cancer Research (2002), 62(15), 4419-4426 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Selective Estrogen Receptor Modulators (SERMs) are a new class of drugs that bind to estrogen receptor (ER) and elicit agonistic or antagonistic responses, depending on the target tissue. We have developed an in vitro system in which some SERMs (4-hydroxytamoxifen and resveratrol) demonstrate estrogenic response through wild-type (wt) ER, whereas others (raloxifene and GW7604) remain antiestrogenic. This system mimics the tamoxifen-resistant phenotype in clinic, when

resistant tumors contain wtER. We used Atlas cDNA arrays to study gene ***expression*** ***profiles*** after ER ***activation*** by ***different*** SERMs in MDA-MB-231 human breast cancer cells stably transfected with wtER. Cells were treated with estradiol, four different SERMs, and the pure antiestrogen ICI 182780. The obtained expression data were analyzed using GeneSpring software. Real-time reverse transcription-PCR was used to verify the array data. Our results showed that treatment with various compds. altered the expression of a diverse group of genes, revealing sets of overlapping genes that may represent a complex network of genes of interrelated signal transduction pathways. Sets of "agonistic" and "antagonistic" genes were identified on the basis of the known response to different SERMs. Further anal. of selected sets of genes revealed functionally related group of genes in each set, encoding proteins that were related to cell proliferation, survival, and apoptosis. Flow cytometry data indicated an antiapoptotic activity in cells treated with agonists vs. apoptotic activity in cells treated with antagonists. A model for estradiol-like (survival) and antiestrogen-like (apoptosis) activities of SERMs on the basis of their gene expression profiles is suggested.
OSC.G 43 THERE ARE 43 CAPLUS RECORDS THAT CITE THIS RECORD (43 CITINGS)
RE.CNT 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 131 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:579759 CAPLUS <<LOGINID::20100206>>
DN 137:259455
TI Proteomics approaches in drug discovery
AU Figeys, Daniel
CS MDS-Proteomics, USA
SO Analytical Chemistry (2002), 74(15), 412A-419A CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal; General Review
LA English
AB A review. The article introduces ***different*** classes of ***proteomics*** and how they are becoming integral to ***drug*** discovery.
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 132 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:540498 CAPLUS <<LOGINID::20100206>>
DN 137:212132
TI Gene expression profile induced by 17.alpha.-ethynyl estradiol, bisphenol A, and genistein in the developing female reproductive system of the rat
AU Naciff, Jorge M.; Jump, M. Lynn; Torontali, Suzanne M.; Carr, Gregory J.; Tiesman, Jay P.; Overmann, Gary J.; Daston, George P.
CS Miami Valley Laboratories, The Procter and Gamble Company, Cincinnati, OH, 45253-8707, USA
SO Toxicological Sciences (2002), 68(1), 184-199 CODEN: TOSCF2; ISSN: 1096-6080
PB Oxford University Press
DT Journal
LA English
AB Exposure to some compds. with estrogenic activity, during fetal development, has been shown to alter development of reproductive organs, leading to abnormal function and disease either after birth or during adulthood. In order to understand the mol. events assocd. with the estrogenicity of different chems. and to det. whether common sets of gene expression changes can be predictive of estrogenic activity, we have used microarray technol. to det. the transcriptional program influenced by exposure to this class of compds. during organogenesis and development. Changes in patterns of gene expression were detd. in the developing uterus and ovaries of Sprague-Dawley rats on GD 20, exposed to graded dosages (s.c.) of 17.alpha.-ethynyl estradiol (EE), genistein, or bisphenol A (BPA) from GD 11 to GD 20. Dose levels were roughly equipotent in estrogenic activity. We compared the transcript profiles between treatment groups and controls, using oligonucleotide arrays to det. the expression level of approx. 7000 rat genes and over 1000 expressed sequence tags (ESTs). At the highest tested doses of EE, BPA, or genistein, we detd. that less than 2% of the mRNA detected by the array showed a 2-fold or greater change in their expression level (increase or decrease). A dose-dependent anal. of the transcript profile revealed a common set of genes whose expression is significantly and reproducibly modified in the same way by each of the 3 chems. tested. Addnl., each compd. induces changes in the expression of other transcripts that are not in common with the others, which indicated not all compds. with estrogenic activity act alike. The results of this study demonstrate that transplacental exposure to chems. with estrogenic ***activity*** ***changes*** the gene ***expression*** ***profile*** of estrogen-sensitive tissues, and that the anal. of the transcript profile of these tissues could be a valuable approach to detg. the estrogenicity of different compds.
OSC.G 101 THERE ARE 101 CAPLUS RECORDS THAT CITE THIS RECORD (101 CITINGS)
RE.CNT 67 THERE ARE 67 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 133 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:531049 CAPLUS <<LOGINID::20100206>>
DN 138:20002
TI Microarray-based expression profiling of normal and malignant immune cells
AU Medh, Rheem D.
CS Department of Biology, California State University at Northridge, Northridge, CA, 91330, USA
SO Endocrine Reviews (2002), 23(3), 393-400 CODEN: ERVIDP; ISSN: 0163-769X
PB Endocrine Society
DT Journal; General Review
LA English
AB A review. Recent advances in gene microarray technol. have facilitated global analyses of gene expression profiles in normal and malignant immune cells. Great strides have been made in our understanding of mol. differences among various types of immune cells, the process of T and B cell activation, and the genomic changes that convert normal cells to malignant ones. Genomic anal. has become a crucial aspect of cancer classification, diagnosis, therapy, and prognosis. This technol. has the potential to reveal the comprehensive transcriptional alterations that dictate fundamental biol. processes such as signal transduction in response to specific stimuli, cell growth, differentiation, and apoptosis. While reaping the benefits of genomic analyses, it is important to realize its limitations with

respect to accuracy of interpretation, reproducibility, and signal detection. It is crucial to optimize signals for individual probe-target pairs and to develop a uniform set of criteria for data analyses. The development of a public-access database of results from individual labs. will pave the way for identifying discrepancies and advancing scientific breakthroughs.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 134 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:495537 CAPLUS <<LOGINID::20100206>>
DN 138:82724
TI Gene-expression-based responses to drug treatment
AU De Backer, Marianne D.; Thurmond, Robin L.; Carmen, Andrew A.; Luyten, Walter H. M. L.
CS Dept. of GI Emerging Diseases, Beerse, B-2340, Belg.
SO Drug News & Perspectives (2002), 15(3), 155-165 CODEN: DNPEED; ISSN: 0214-0934
PB Prous Science
DT Journal; General Review
LA English
AB A review. Perfect drugs are potent, specific and nontoxic. Many compds. fail because of unexpected toxicity and lack of efficacy in later stages of clin. development. Therefore, more complete knowledge and understanding of the properties of a drug is needed at an earlier stage of drug development. DNA microarrays can yield gene expression profiles from cells or tissues treated with a compd. Such expression fingerprints are used in drug discovery for drug target identification and validation and for elucidating the mode of action of novel compds. during lead identification and optimization. Moreover, during drug development, DNA microarrays help in the discovery of new diagnostic and prognostic biomarkers, as well as in the prediction of resistance and toxic side effects. This review aims to assess to what extent the promise of gene ***expression*** ***profiling*** has already materialized for the ***different*** stages of ***drug*** discovery and development.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 69 THERE ARE 69 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 135 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:479038 CAPLUS <<LOGINID::20100206>>
DN 138:101239
TI Transcriptional program of mouse osteoclast differentiation governed by the macrophage colony-stimulating factor and the ligand for the receptor activator of NF.kappa.B
AU Cappellen, David; Luong-Nguyen, Ngoc-Hong; Bongiovanni, Sandrine; Grenet, Olivier; Wanke, Christoph; Susa, Mira
CS Arthritis and Bone Metabolism Therapeutic Area, Novartis Pharma Research, Basel, CH-4002, Switz.
SO Journal of Biological Chemistry (2002), 277(24), 21971-21982 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Cytokines macrophage colony stimulating factor (M-CSF) and the receptor activator of NF.kappa.B ligand (RANKL) induce differentiation of bone marrow hematopoietic precursor cells into bone-resorbing osteoclasts without the requirement for stromal cells of mesenchymal origin. We used this recently described mouse cell system and oligonucleotide microarrays representing about 9,400 different genes to analyze gene expression in hematopoietic cells undergoing differentiation to osteoclasts. The ability of microarrays to detect the genes of interest was validated by showing expression and expected regulation of several osteoclast marker genes. In total 750 known transcripts were up-regulated by .gtoreq.2-fold, and 91% of them at an early time in culture, suggesting that almost the whole differentiation program is defined already in pre-osteoclasts. As expected, M-CSF alone induced the receptor for RANKL (RANK), but also, unexpectedly, other RANK/NF.kappa.B pathway components (TRAF2A, PI3-kinase, MEKK3, RIPK1), providing a mol. explanation for the synergy of M-CSF and RANKL. Furthermore, interleukins, interferons, and their receptors (IL-1.alpha., IL-18, IFN-.beta., IL-11R.alpha.2, IL-6/11R gp130, IFN.gamma.R) were induced by M-CSF. Although interleukins are thought to regulate osteoclasts via modulation of M-CSF and RANKL expression in stromal cells, we showed that a mix of IL-1, IL-6, and IL-11 directly increased the activity of osteoclasts by 8.5-fold. RANKL induced about 70 novel target genes, including chemokines and growth factors (RANTES (regulated on activation, normal T cell expressed and secreted), PDGF.alpha., IGF1), histamine, and .alpha.1A-adrenergic receptors, and three waves of distinct receptors, transcription factors, and signaling mols. In conclusion, M-CSF induced genes necessary for a direct response to RANKL and interleukins, while RANKL directed a three-stage differentiation program and induced genes for interaction with osteoblasts and immune and nerve cells. Thus, global gene expression suggests a more dynamic role of osteoclasts in bone physiol. than previously anticipated.
OSC.G 71 THERE ARE 71 CAPLUS RECORDS THAT CITE THIS RECORD (71 CITINGS)
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 136 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:476808 CAPLUS <<LOGINID::20100206>>
DN 137:58705
TI Mode of action of chlorinated ethylenes on the expression of rat cytochrome P450 forms and specificity in the metabolic activation of CEs by CYPs
AU Inouye, Yoshio
CS Sch. Pharm. Sci., Toho Univ., Funabashi, 274-8510, Japan
SO Journal of Health Science (2002), 48(3), 223-226 CODEN: JHSCFD; ISSN: 1344-9702
PB Pharmaceutical Society of Japan
DT Journal; General Review
LA English
AB A review. Chlorinated ethylenes (CEs) including tetrachloroethylene (PCE), trichloroethylene (TCE) and 1,1-dichloroethylene (DCE) were comparatively evaluated for their effects on the expression of cytochrome P 450 (CYP) forms of subfamilies 1A, 2B, 2E and 3A as well as their relative suitability as substrates of these CYPs. The magnitudes of inhibition of the enzyme activities were as follows in descending order: 1,1-DCE > TCE > PCE against hepatic CYPs and PCE > 1,1-DCE > TCE against pulmonary CYP2B1. These organ-specific profiles in the sensitivities to the adverse effects of CEs were partly attributable to the ***differential*** ***expression*** ***patterns*** of CYP forms by which they were metabolically ***activated*** . The expression of hepatic and pulmonary

CYP2B mRNA was severely suppressed in the presence of 1,1-DCE during the entire observation period until 30 h after the CE-treatment, in marked contrast to the temporarily enhanced expression at 6 h followed by a moderate suppression in the cases of PCE and TCE with the trough values being obsd. at 18 h. In addn. to CYP2B, 1,1-DCE in advance of the transcriptional stage, when simultaneously treated with phenobarbital, also exclusively suppressed CYP2E1. These general suppressive effects of 1,1-DCE on the expression of divergent CYP mRNAs in vivo resembled the published findings in primary cultured hepatocytes treated with inflammatory cytokines such as IL-1.beta., TNF-.alpha. and IL-6, implying the highly inflammatory nature of 1,1-DCE.

L12 ANSWER 137 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:468634 CAPLUS <<LOGINID::20100206>>
DN 137:43637
TI Detection technologies in proteome analysis
AU Patton, Wayne F.
CS Proteomics Section, Biosciences Department, Molecular Probes, Inc., Eugene, OR, 97402-9165, USA
SO Journal of Chromatography, B: Analytical Technologies in the Biomedical and Life Sciences (2002), 771(1-2), 3-31 CODEN: JCBAAI; ISSN: 1570-0232
PB Elsevier Science B.V.
DT Journal; General Review
LA English
AB A review. Common strategies employed for general protein detection include org. dye, silver stain, radiolabeling, reverse stain, fluorescent stain, chemiluminescent stain and mass spectrometry-based approaches. Fluorescence-based protein detection methods have recently surpassed conventional technologies such as colloidal Coomassie blue and silver staining in terms of quant. accuracy, detection sensitivity, and compatibility with modern downstream protein identification and characterization procedures, such as mass spectrometry. Addnl., specific detection methods suitable for revealing protein post-translational modifications have been devised over the years. These include methods for the detection of glycoproteins, phosphoproteins, proteolytic modifications, S-nitrosylation, arginine methylation and ADP-ribosylation. Methods for the detection of a range of reporter enzymes and epitope tags are now available as well, including those for visualizing .beta.-glucuronidase, .beta.-galactosidase, oligohistidine tags and green fluorescent protein. Fluorescence-based and mass spectrometry-based methodologies are just beginning to offer unparalleled new capabilities in the field of proteomics through the performance of multiplexed quant. anal. The primary objective of differential display proteomics is to increase the information content and throughput of proteomics studies through multiplexed anal. Currently, three principal approaches to ***differential*** display ***proteomics*** are being ***actively*** pursued, ***difference** gel electrophoresis (DIGE), multiplexed ***proteomics*** (MP) and isotope-coded affinity tagging (ICAT). New multiplexing capabilities should greatly enhance the applicability of the two-dimensional gel electrophoresis technique with respect to addressing fundamental questions related to proteome-wide changes in protein expression and post-translational modification.
OSC.G 285 THERE ARE 285 CAPLUS RECORDS THAT CITE THIS RECORD (285 CITINGS)
RE.CNT 204 THERE ARE 204 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 138 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:442967 CAPLUS <<LOGINID::20100206>>
DN 137:15103
TI Pharmaco-proteomics based on structural biology
AU Ishiguro, Masaji
CS Suntory Inst. Bioorg. Res., Japan
SO Tanpakushitsu Kakusan Koso (2002), 47(8, Zokan), 960-966 CODEN: TAKKAJ; ISSN: 0039-9450
PB Kyoritsu Shuppan
DT Journal; General Review
LA Japanese
AB A review on drug design based on the structure proteomics and computer simulation, discussing structure ***proteomics*** and stereostructure estn. in ***drug*** discovery, function-related conformation ***changes*** in ***drug*** targeting proteins such as enzymes, membrane proteins, and ion channel and transporters, and drug design based on anal. of their dynamic conformation changes.

L12 ANSWER 139 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:426617 CAPLUS <<LOGINID::20100206>>
DN 137:1581
TI Modulating gene expression in insects by using double-stranded RNA (dsRNA)
IN Gunkel, Nikolas
PA Aventis CropScience GmbH, Germany
SO Eur. Pat. Appl., 26 pp. CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI EP 1210875 A1 20020605 EP 2000-126632 20001204 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR WO 2002046432 A2 20020613 WO 2001-EP13657 20011123 WO 2002046432 A3 20021017 W: AE, AG, AL, AM, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CN, CO, CR, CU, CZ, DM, DZ, EC, EE, GD, GE, HR, HU, ID, IL, IN, IS, JP, KG, KP, KR, KZ, LC, LK, LR, LT, LV, MA, MD, MG, MK, MN, MX, NO, NZ, OM, PH, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, US, UZ, VN, YU, ZA RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002019140 A 20020618 AU 2002-19140 20011123 PRAI EP 2000-126632 A 20001204 WO 2001-EP13657 W 20011123
AB The invention relates to the identification of target mols. arthropods for insecticides or acaricides. Target genes of interest encoding such target mols. are esp. genes that are ***active*** /inactive or show at least ***different*** ***expression*** ***profiles*** esp. according to specific developmental stages/life cycles. The identification of these new insecticidal target sites is practiced by using double-stranded RNA (dsRNA) mols. for targeting specific genes in transgenic flies.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 140 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2002:419919 CAPLUS <<LOGINID::20100206>>
DN 137:276110
TI Keeping killers on a tight leash: transcriptional and post-translational control of the pro-apoptotic activity of BH3-only proteins
AU Puthalakath, H.; Strasser, A.
CS The Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
SO Cell Death and Differentiation (2002), 9(5), 505-512 CODEN: CDDIEK; ISSN: 1350-9047
PB Nature Publishing Group
DT Journal; General Review
LA English
AB A review. BH3-only proteins are structurally distant members of the Bcl-2 protein family that trigger apoptosis. Genetic expts. have shown that these proteins are essential initiators of programmed cell death in species as distantly related as mice and C. elegans. BH3-only proteins share with each other and with the remainder of the Bcl-2 family only a nine amino acid BH3 (Bcl-2 Homol.) region. Mutational analyses have demonstrated that this domain is required for their ability to bind to Bcl-2-like pro-survival proteins and to initiate apoptosis. So far only one BH3-only protein, EGL-1, has been identified in C. elegans and it is required for all developmentally programmed death of somatic cells in this species. In contrast, mammals have at least 10 BH3-only proteins that ***differ*** in their ***expression*** ***pattern*** and mode of ***activation*** . Studies in gene targeted mice have indicated that different BH3-only proteins are required for the initiation of distinct apoptotic stimuli. The pro-apoptotic activities of BH3-only proteins are stringently controlled by a variety of mechanisms. C. elegans egl-1 as well as mammalian hrk/dp5, noxa, puma/bbc3 and bim/bod are regulated by a diverse range of transcription factors. Certain BH3-only proteins, including Bad, Bik/Nbk, Bid, Bim/Bod and Bmf, are restrained by post-translational modifications that cause their sequestration from pro-survival Bcl-2 family members. In this review we describe current knowledge of the functions and transcriptional as well as post-translational control mechanisms of BH3-only proteins.
OSC.G 383 THERE ARE 383 CAPLUS RECORDS THAT CITE THIS RECORD (383 CITINGS)
RE.CNT 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 141 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:396057 CAPLUS <<LOGINID::20100206>>
DN 137:362845
TI Gene ***expression*** ***profile*** of adipocyte ***differentiation*** and its regulation by peroxisome proliferator- ***activated*** receptor-.gamma. agonists
AU Gerhold, David L.; Liu, Franklin; Jiang, Guoqiang; Li, Zhihua; Xu, Jian; Lu, Meiqing; Sachs, Jeffrey R.; Bagchi, Ansuman; Fridman, Arthur; Holder, Daniel J.; Doebber, Thomas W.; Berger, Joel; Elbrecht, Alex; Moller, David E.; Zhang, Bei B.
CS Department of Pharmacology, Merck Research Laboratories, Rahway, NJ, 07065, USA
SO Endocrinology (2002), 143(6), 2106-2118 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB PPAR.gamma. is an adipocyte-specific nuclear hormone receptor. Agonists of PPAR.gamma., such as thiazolidinediones (TZDs), promote adipocyte differentiation and have insulin-sensitizing effects in animals and diabetic patients. Affymetrix oligonucleotide arrays representing 6347 genes were employed to profile the gene expression responses of mature 3T3-L1 adipocytes and differentiating preadipocytes to a TZD PPAR.gamma. agonist in vitro. The expression of 579 genes was significantly up- or down-regulated by more than 1.5-fold during differentiation and/or by treatment with TZD, and these genes were organized into 32 clusters that demonstrated concerted changes in expression of genes controlling cell growth or lipid metab. Quant. PCR was employed to further characterize gene expression and led to the identification of .beta.-catenin as a new PPAR.gamma. target gene. Both mRNA and protein levels for .beta.-catenin were down-regulated in 3T3-L1 adipocytes compared with fibroblasts and were further decreased by treatment of adipocytes with PPAR.gamma. agonists. Treatment of db/db mice with a PPAR.gamma. agonist also resulted in redn. of .beta.-catenin mRNA levels in adipose tissue. These results suggest that .beta.-catenin plays an important role in the regulation of adipogenesis. Thus, the transcriptional patterns revealed in this study further the understanding of adipogenesis process and the function of PPAR.gamma. activation.
OSC.G 82 THERE ARE 82 CAPLUS RECORDS THAT CITE THIS RECORD (82 CITINGS)
RE.CNT 64 THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 142 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:393634 CAPLUS <<LOGINID::20100206>>
DN 137:245176
TI The role of expression of extracellular matrix proteins and epidermal growth factor receptor activity on fertilization capacity of testicular harvested spermatozoa
AU Erdogru, T.; Gulkesen, K. H.; Bahceci, M.; Karpuzoglu, G.; Baykara, M.
CS Department of Urology, Akdeniz University Faculty of Medicine, Antalya, 07059, Turk.
SO Andrologia (2002), 34(2), 98-106 CODEN: ANDRDQ; ISSN: 0303-4569
PB Blackwell Verlag
DT Journal
LA English
AB It has been suggested that multiple growth factors are crucial for spermatogenesis. We analyzed whether alterations on epidermal growth factor receptor ***activity*** and ***different*** ***expression*** ***pattern*** of extracellular matrix proteins had an impact on the fertilization capacity of spermatozoa and pregnancy rate after testicular sperm extn. and intracytoplasmic injection. Extracellular matrix proteins and epidermal growth factor receptor were immunohistochem. evaluated in testis of 88 patients with nonobstructive azoospermia. Testicular sperm extn. and intracytoplasmic injection procedure was also performed in 32 of the patients for whom mature sperm could be harvested from the testicular tissue. While collagen Type-IV and laminin activity percentages were 33.1% and 86.4% in motile sperm harvested testicular tissue, these activities were 23.3% and 89.3% in immotile sperm harvested testicular tissue, resp. In addn., the mean epidermal growth factor receptor expression was higher in immotile than motile sperm obtained tissue (56.4% vs. 51.1%, P=0.4928). There was no statistically significant relationship between the extracellular matrix protein and epidermal growth factor receptor expression patterns and sperm motility, fertilization and pregnancy rates in testicular sperm extn. and intracytoplasmic injection. However, further studies are required

to investigate the relationship between other growth factors and sperm fertilization capacity.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 143 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:392751 CAPLUS <<LOGINID::20100206>>
DN 138:13044
TI Inhibition of calcineurin and sarcolemmal Ca2+ influx protects cardiac morphology and ventricular function in Kv4.2N transgenic mice
AU Sah, Rajan; Oudit, Gavin Y.; Nguyen, The-Tin T.; Lim, Hae W.; Wickenden, Alan D.; Wilson, Gregory J.; Molkentin, Jeffery D.; Backx, Peter H.
CS Dep. of Laboratory Medicine and Pathobiology, University of Toronto, University Health Network, Toronto, ON, M5S 3EZ, Can.
SO Circulation (2002), 105(15), 1850-1856 CODEN: CIRCAZ; ISSN: 0009-7322
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB Background - Cardiac-targeted expression of truncated Kv4.2 subunit (Kv4.2N) reduces transient outward current (Ito) d., prolongs action potentials (APs), and enhances contractility in 3- to 4-wk-old transgenic mice. By 13 to 15 wk of age, these mice develop severely impaired cardiac function and signs of heart failure. In this study, we examd. whether augmented contractility in Kv4.2N mice results from elevations in intracellular calcium ([Ca2+]i) secondary to AP prolongation and investigated the putative roles of calcineurin activation in heart disease development of Kv4.2N mice. Methods and Results - At 3 to 4 wk of age, L-type Ca2+ influx and peak [Ca2+]i were significantly elevated in Kv4.2N myocytes compared with control because of AP prolongation. Cardiac calcineurin activity was also significantly elevated in Kv4.2N mice by 5 wk of age relative to controls and increased progressively as heart disease developed. This was assocd. with activation of protein kinase C (PKC)-.alpha. and PKC-.theta. but not PKC-.epsilon., as well as increases in .beta.-myosin heavy chain (.beta.-MHC) and redns. in sarcoplasmic/endoplasmic reticulum Ca2+-ATPase (SERCA)-2a expression. Treatment with either cyclosporin A or verapamil prevented increases in heart wt. to body wt. ratios, interstitial fibrosis, impaired contractility, PKC ***activation*** , and ***changes*** in the ***expression*** ***patterns*** of .beta.-MHC and SERCA2a. Conclusions - Our results demonstrate that AP prolongation caused by Ito redn. results in enhanced Ca2+ cycling and hypercontractility in mice and suggests that elevations in [Ca2+]i via ICa,L, and activation of calcineurin play a central role in disease development after Ito redn. using the Kv4.2N construct.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 144 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:374924 CAPLUS <<LOGINID::20100206>>
DN 137:350144
TI Screening of gene expression profiles in gastric epithelial cells induced by Helicobacter pylori using microarray analysis
AU Sepulveda, A. R.; Tao, H.; Carloni, E.; Sepulveda, J.; Graham, D. Y.; Peterson, L. E.
CS Department of Pathology, University of Pittsburgh, Pittsburgh, PA, 15213-2582, USA
SO Alimentary Pharmacology and Therapeutics (2002), 16(Suppl. 2), 145-157 CODEN: APTHEN; ISSN: 0269-2813
PB Blackwell Publishing Ltd.
DT Journal
LA English
AB H. pylori infection is a major risk factor in gastric cancer development. The availability of cDNA microarrays creates the unprecedented opportunity to examine simultaneously dynamic changes of multiple pathways affected by H. pylori infection. In this study we examd. broad patterns of gene expression induced by H. pylori in the gastric cancer cell line 1739-CRL AGS cells in culture using the U95A microarray. H. pylori were cocultured with AGS cells for 4, 12, 24 and 48 h. Total RNA was extd. and after labeling was used for detection of genes represented in the human U95A microarray set. Data analyses were performed using GeneChip and CLUSFAVOR software. Nearly 6000 genes present in the array were expressed by AGS cells. We report approx. 200 genes that showed the most marked changes. Our studies confirm the up-regulation of c-jun, jun-B, c-fos and cyclin D1 by H. pylori. We report for the first time the induction of the serine threonine kinase pim-1 and ATF3 by H. pylori infection of AGS cells. In this microarray anal. of gene expression induced by H. pylori in gastric epithelial cells, we identified a large no. of unsuspected genes affected by H. pylori. Further, we show that unsupervised hierarchical cluster anal. can provide useful insight into the possible contribution of genes in specific pathways, based on their profile of expression.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 145 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:371141 CAPLUS <<LOGINID::20100206>>
DN 137:106114
TI Body shaping under water stress: osmosensing and osmoregulation of solute transport in bacteria
AU Morbach, Susanne; Kramer, Reinhard
CS Institut fur Biochemie der Universitat zu Koln, Koln, 50674, Germany
SO ChemBioChem (2002), 3(5), 384-397 CODEN: CBCHFX; ISSN: 1439-4227
PB Wiley-VCH Verlag GmbH
DT Journal; General Review
LA English
AB A review. Fluctuation of external osmolarity is one of the most common types of environmental stress factors for all kind of cells, both of prokaryotic and of eukaryotic origin. Cells try to keep their vol. and/or turgor pressure const.; consequently, both a decrease (hypoosmotic stress) and an increase (hyperosmotic stress) of the solute concn. (correctly: increase or decrease in water activity) in the surrounding area resp., are challenges for cellular metab. and survival. A common example from the prokaryotic world is the fate of a soil bacterium that after a sunny day has dried out the soil (hyperosmotic stress), is suddenly exposed to a drop of distd. water from a rain cloud (hypoosmotic stress). The immediate and inevitable passive response to the sudden osmotic shift in the surroundings is fast water efflux out of the cell in the former situation and water influx in the latter. In the worst case these responses may lead to either loss of cell

turgor and plasmolysis or to cell burst. In order to overcome such drastic consequences cells have developed effective mechanisms, namely osmoadaptation, to cope with the two different types of osmotic stress. For a graded reaction to osmotic shifts, cells must be able (1) to sense stimuli related to osmotic stress, (2) to transduce corresponding signals to those systems that properly respond (3) by ***activating*** transport or enzymic functions or (4) by ***changing*** gene ***expression***. ***profiles***. In this review membrane proteins involved in the cell's active response to osmotic stress are described. Mol. details of structure, function, and regulation of mechanosensitive efflux channels from various organisms, as well as of osmoregulated uptake systems are discussed.
CSC.G 41 THERE ARE 41 CAPLUS RECORDS THAT CITE THIS RECORD (41 CITINGS)
RE.CNT 107 THERE ARE 107 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 146 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:362282 CAPLUS<<LOGINID::20100206>>
DN 137:119863
TI Guinea Pig Gonadotropin-Releasing Hormone: Expression Pattern, Characterization and Biological Activity in Rodents
AU Montaner, Alejandro D.; Mongiat, Lucas; Lux-Lantos, Victoria A.; Warby, Carol; Chewpoy, Brad; Bianchi, Maria S.; Libertun, Carlos; Rivier, Jean E.; Sherwood, Nancy M.; Somoza, Gustavo M.
CS Instituto de Investigaciones Biomedicas, Fundacion Pablo Cassara, Buenos Aires, Argent.
SO Neuroendocrinology (2002), 75(5), 326-338 CODEN: NUNDAJ; ISSN: 0028-3835
PB S. Karger AG
DT Journal
LA English
AB Gonadotropin-releasing hormone (GnRH) is a decapeptide widely known for its role in regulating vertebrate reprodn. by serving as a signal from the hypothalamus to pituitary gonadotropes. The first form of GnRH to be identified was isolated from mammals (mGnRH) and the same form has been reported for all mammals studied, which includes marsupials and placental mammals. Later, another variant, chicken GnRH-II (cGnRH-II) was shown to be expressed together with mGnRH in the brains of all jawed vertebrates, including mammals such as rats, monkeys and humans. Our objective was to characterize a third form of GnRH that was isolated previously as mRNA from guinea pigs (gpGnRH), but has not been reported for any other mammal to date. Furthermore, the gonadotropic activity of gpGnRH has not been fully characterized. Our results, using chromatog. and immunol. methods, show for the first time that gpGnRH is expressed together with mGnRH in some rodents (wild guinea pig and capybara), but not in others (mouse and hamster). Also, the gonadotropic activity of gpGnRH and mGnRH was tested in two different rat cell culture systems. Although there have been reports that the salmon(s) form of GnRH is present in mammals, we did not detect sGnRH in capybara, wild guinea pigs, hamsters, rats or mice. Taken together with previous reports, the present results support the idea that the expression of multiple GnRH variants in a single species is a common pattern in most vertebrate groups.
CSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 147 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:355225 CAPLUS<<LOGINID::20100206>>
DN 137:304595
TI Differential gene regulation by PPAR.gamma. agonist and constitutively active PPAR.gamma.2
AU Li, Yong; Lazar, Mitchell A.
CS Division of Endocrinology, Diabetes, and Metabolism, Departments of Medicine and Genetics, and The Penn Diabetes Center, University of Pennsylvania School of Medicine, Philadelphia, PA, 19104, USA
SO Molecular Endocrinology (2002), 16(5), 1040-1048 CODEN: MOENEN; ISSN: 0888-8809
PB Endocrine Society
DT Journal
LA English
AB The PPAR.gamma. is a key adipogenic detn. factor. Ligands for PPAR.gamma. such as antidiabetic thiazolidinedione (TZD) compds. are adipogenic, and many adipocyte genes that are activated by TZDs contain binding sites for PPAR.gamma.. Like ligands for other nuclear receptors, TZDs can regulate genes pos. or neg. Here, the authors sought to understand the importance of pos. regulation of gene expression by PPAR.gamma. in adipogenesis. Fusion of the potent viral transcriptional activator VP16 to PPAR.gamma.2 (VP16-PPAR.gamma.) created a transcription factor that constitutively and dramatically activated transcription of PPAR.gamma.-responsive genes in the absence of ligand. Forced expression of VP16-PPAR.gamma. in 3T3-L1 preadipocytes using retroviral vectors led to adipogenesis in the absence of std. differentiating medium or any exogenous PPAR.gamma. ligand. Gene microarray anal. revealed that VP16-PPAR.gamma. induced many of the genes assocd. with adipogenesis and adipocyte function. Thus, direct up-regulation of gene expression by PPAR.gamma. is sufficient for adipogenesis. TZD-induced adipogenesis up-regulated many of the same genes, although some were divergently regulated, including resistin, whose gene expression was reduced inVP16-PPAR.gamma. adipocytes treated with TZDs. These results show that, although activation of PPAR.gamma. by a heterologous activation domain is sufficient for adipogenesis, it is not equiv. to TZD treatment. This conclusion has important implications for understanding biol. effects of the TZDs on adipogenesis and insulin sensitization.
CSC.G 46 THERE ARE 46 CAPLUS RECORDS THAT CITE THIS RECORD (46 CITINGS)
RE.CNT 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 148 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:353659 CAPLUS<<LOGINID::20100206>>
DN 136:364971
TI Human gene Del-1 differentially expressed in benign prostatic hyperplasia and its use in diagnosis and drug screening
IN Munger, William E.; Kulkarni, Prakash; Getzenberg, Robert H.
PA Gene Logic, Inc., USA; Japan Tobacco, Inc.
SO PCT Int. Appl., 41 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------

PI WO 2002036826 A2 20020510 WO 2001-US42915 20011105 WO 2002036826 A3 20031120 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002032403 A 20020515 AU 2002-32403 20011105
PRAI US 2000-245674P P 20001106 WO 2001-US42915 W 20011105
AB The invention relates generally to the changes in gene expression in Benign Prostatic Hyperplasis (BPH). The invention relates specifically to the human gene Del-1 which is differentially expressed in BPH compared to normal prostate tissue. The cloned cDNA is useful for BPH diagnosis and drug screening.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 149 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:339284 CAPLUS <<LOGINID::20100206>>
DN 138:33258
TI Activation of the nuclear transcription factor .kappa.B (NF.kappa.B) and differential gene expression in U87 glioma cells after exposure to the cytoprotecter amifostine
AU Kataoka, Yasushi; Murley, Jeffrey S.; Khodarev, Nikolai N.; Weichselbaum, Ralph R.; Grdina, David J.
CS Department of Radiation and Cellular Oncology, University of Chicago, Chicago, IL, USA
SO International Journal of Radiation Oncology, Biology, Physics (2002), 53(1), 180-189 CODEN: IOBPD3; ISSN: 0360-3016
PB Elsevier Science Inc.
DT Journal
LA English
AB Purpose: Amifostine has been approved as a therapy to decrease the incidence of moderate-to-severe xerostomia in patients undergoing postoperative radiation treatment for head-and-neck cancer. As a reducing agent capable of participating in intracellular reductive/oxidative processes, it has the potential to affect redox-sensitive transcription factors and gene expression. Amifostine's active free thiol WR-1065 was investigated to det. its effect on nuclear transcription factor .kappa.B (NF.kappa.B) activation and subsequent gene expression in U87 glioma cells. Methods and Materials: The human glioma cell line U87 was grown to confluency and then exposed to WR-1065 at a concn. of 40 .mu.M for times ranging from 30 min to 24 h. Changes in cell cycle were monitored by flow cytometry. The effect of WR-1065 on NF.kappa.B activation was detd. by a gel shift assay. Changes in gene expression as a function of time of exposure to WR-1065 were detd. by Northern blot and the Atlas Human cDNA Expression Array (Contech, Palo Alto, CA). Changes in gene expression using the Atlas Array were verified by reverse transcriptase-polymerase chain reaction (RT-PCR) with gene-specific primers. Results: Exposure of U87 cells to 40 .mu.M WR-1065 resulted in a marked activation of NF.kappa.B between 30 min and 1 h after treatment. Expression of MnSOD, an NF.kappa.B-responsive gene, was enhanced by over 2-fold after 16 h of treatment and remained elevated at 24 h. During this period of time, no changes in cell cycle distribution were obsd. To assess changes in the expression levels of NF.kappa.B-responsive genes as a function of WR-1065 exposure, cDNA arrays contg. 49 genes identified as having DNA-binding motifs for NF.kappa.B were used. Only five genes were found to be significantly affected at 1, 4, and/or 16 h of treatment. GST-3 and c-myc were repressed up to 2- and 4-fold, resp. The expression levels of IL-2Rα, RANTES, and c-myb, in contrast, were enhanced up to 14-, 3-, and 2-fold, resp. The remaining genes having NF.kappa.B-responsive elements in their promoter regions were either not expressed (20 genes) or were not affected (24 genes) by exposure to WR-1065. Conclusions: The redox-sensitive transcription factor NF.kappa.B can be activated in U87 glioma cells by the active thiol form of the cytoprotector amifostine. Activation of NF.kappa.B by the antioxidant WR-1065 is accompanied by a reduced expression of the oncogene c-myc and an enhanced expression of the antioxidant gene MnSOD, a gene whose expression in tumor cells is relatively low, but when overexpressed has been correlated with a suppression of the malignant phenotype. Activation of NF.kappa.B by WR-1065, however, results in selective rather than global changes in the expression of genes contg. NF.kappa.B-responsive elements.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 150 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:334080 CAPLUS <<LOGINID::20100206>>
DN 137:60665
TI Species differences in the distribution of drug-metabolizing enzymes in the pancreas
AU Ulrich, Alexis B.; Standop, Jens; Schmied, Bruno M.; Schneider, Matthias B.; Lawson, Terence A.; Pour, Parviz M.
CS UNMC Eppley Cancer Center, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SO Toxicologic Pathology (2002), 30(2), 247-253 CODEN: TOPADD; ISSN: 0192-6233
PB Taylor & Francis
DT Journal
LA English
AB We investigated the cellular expression of 9 cytochrome P 450-isoenzymes (CYP1A1, CYP1A2, CYP2B6, CYP2C8,9,19, CYP2D1, CYP2E1, CYP3A1, CYP3A2, CYP3A4) and 3 glutathione S-transferase-isoenzymes (GST-.pi., GST-.alpha., GST-.mu.) in the pancreas of hamsters, mice, rats, rabbits, pigs, dogs and monkeys, and in comparison with the human pancreas. A wide variation was found in the cellular localization of these enzymes between the 8 species. Most enzymes were expressed in the pancreas of the hamster, mouse, monkey and human, whereas rats, pigs, rabbits and dogs were lacking several isoenzymes. However, in all of the species the islet cells expressed more enzymes than ductal and acinar cells. An exclusive expression of enzymes in the islet cells was found in the hamster (CYP2E1), mouse (CYP1A1, CYP1A2, GST-.alpha., GST-.mu.), rat (CYP2C8,9,19), rabbit (CYP1A2, CYP2B6, GST-.pi.), and pig (CYP1A1). Although no polymorphism was found in the pancreas of animals, in human tissue four enzymes were missing in about 50% of the cases. The results imply a greater importance of the islet cells in the metab. of xenobiotics within the pancreas. The differences in the distribution of these drug-metabolizing enzymes in the pancreas between the species call for caution when extrapolating exptl. results to humans.

OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 151 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:325328 CAPLUS <<LOGINID::20100206>>
DN 137:166595
TI Gene expression changes in response to E2F1 activation
AU Stanelle, Jens; Stiewe, Thorsten; Theseling, Carmen C.; Peter, Martin; Puetzer, Brigitte M.
CS Centre for Cancer Research and Cancer Therapy, Institute of Molecular Biology, University of Essen, Medical School, Essen, D-45122, Germany
SO Nucleic Acids Research (2002), 30(8), 1859-1867 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The p16/RB/E2F regulatory pathway, which controls transit through the G1 restriction point of the cell cycle, is one of the most frequent targets of genetic alterations in human cancer. Any of these alterations results in the deregulated expression of the transcription factor E2F, one of the key mediators of cell cycle progression. Under these conditions, E2F1 also participates in the induction of apoptosis by a p53-dependent pathway, and independently of p53. Recently, we identified the p53-homolog p73 as a first direct target of p53-independent apoptosis. Here, we used a cDNA microarray to screen an inducible E2F1-expressing Saos-2 cell line for E2F1 target genes. Expression anal. by cDNA microarray and RT-PCR revealed novel E2F1 target genes involved in E2F1-regulated cellular functions such as cell cycle control, DNA replication and apoptosis. In addn., the identification of novel E2F1 target genes participating in the processes of angiogenesis, invasion and metastasis supports the view that E2F1 plays a central role in many aspects of cancer development. These results provide new insight into the role of E2F1 in tumorigenesis as a basis for the development of novel anti-cancer therapeutics.
OSC.G 82 THERE ARE 82 CAPLUS RECORDS THAT CITE THIS RECORD (82 CITINGS)
RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 152 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:250062 CAPLUS <<LOGINID::20100206>>
DN 136:228822
TI Proteomics in clinical research: New approach of mass spectrometry
AU Shimizu, Akira; Nakanishi, Toyohumi; Koyama, Reiko; Ikeda, Tsunehiko
CS Dep. Clin. Pathol., Osaka Med. Coll., Takatsuki, 569-8686, Japan
SO Rinsho Byori (2002), 50(2), 169-172 CODEN: RBYOAI; ISSN: 0047-1860
PB Nippon Rinsho Kensa Igakkai
DT Journal; General Review
LA Japanese
AB A review. A proteome has been defined as the protein complement expressed by the genome of an organism, tissue, or differentiated cell. Knowledge of complete genome sequences has led to considerable effort being increasingly devoted to the large-scale study of proteomes, i.e., 'proteomics'. Commonly, two ***proteomes*** are compared by a substructive anal. in which ***differences*** due to ***drug*** treatment, culture conditions, genetic variations, or diseases can be obsd. Two-dimensional gel electrophoresis and mass spectrometry are commonly used for the purpose. We applied this approach to the anal. of vitreous humor (VH) proteins. Fifty-two different proteins were identified on silver-stained 2D-gel patterns with VH proteins obtained from diabetic retinopathy and macular hole. Thirty-five proteins, which have not reported in plasma, were found in VH. Pigment epithelium-derived factor, which was reported to be a potent inhibitor of angiogenesis in cornea and vitreous was at a higher concn. in VH with diabetes than in that with macular hole. It is impressive that the inhibitor increases in the vitreous with proliferative angiogenesis. Unique applications in proteomics promise a bright future for mol. biol. and hopefully for clin. chem.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L12 ANSWER 153 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:226262 CAPLUS <<LOGINID::20100206>>
DN 137:104697
TI Differential gene expression profiles of Jnk1- and Jnk2-deficient murine fibroblast cells
AU Chen, Nanyue; She, Qing-Bai; Bode, Ann M.; Dong, Zigang
CS The Hormel Institute, University of Minnesota, Austin, MN, 55912, USA
SO Cancer Research (2002), 62(5), 1300-1304 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB C-Jun NH2-terminal kinase (JNK) 1 and JNK2 have been assumed to complement each other and mediate the same or similar biol. functions. However, our recent reports indicated that 7,12-dimethylbenz(a)anthracene/12-O-tetradecanoylphorbol-13-acetate-induced tumor development is suppressed in Jnk2 knockout mice but enhanced in Jnk1 knockout mice. In the present work, primary embryo cells were isolated from wild-type, Jnk1-/- and Jnk2-/- mice and used for cDNA microarray anal. The patterns of gene expression in Jnk1-/-, Jnk2-/-, and wild-type cells are different. After 12-O-tetradecanoylphorbol-13-acetate treatment, the changes in the gene expression profiles in three different kinds of cells appear to agree with the differences in susceptibility to tumorigenesis of each resp. animal model. These results suggest that JNK1 and JNK2 proteins have different roles in modulating cell function.
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 154 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:224824 CAPLUS <<LOGINID::20100206>>
DN 137:104335
TI Matching gene activity with physiological functions
AU Huang, Wei; Sher, Yuh-Pyng; Peck, Konan; Fung, Yuan Cheng B.
CS Department of Bioengineering, University of California at San Diego, La Jolla, CA, 92093-0412, USA

SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(5), 2603-2608 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Matching the activity of the genes with biomechanics and physiol. is an effective way to use cDNA microarray technol. Required are data on the change of activities of genes assocd. with specific physiol. functions with respect to a continuous variable such as time. For each pair of data (gene and physiol. function) as functions of time, we can compute a coeff. of correlation, R. The correlation is perfect if R is +1 or -1; it is nonexistent if R = 0. By evaluating R for every gene in a microarray, we can arrange the genes in the order of the no. R, thus learning which genes are best correlated with the mech. or physiol. function. We illustrate this procedure by studying the blood vessels in the lung in response to pulmonary hypoxic hypertension, including the remodeling of vascular morphometry, the elastic moduli, and the zero-stress state of the vessel wall. For each physiol. function, we identify the top genes that correlate the best. We found that different genes correlate best with a given function in large and small arteries, and that the genes in pulmonary veins which respond to arterial functions are different from those in pulmonary arteries. We found one set of genes matching the remodeling of arterial wall thickness, but another set of genes whose integral of activity over time best fit the wall thickness change. Our method can be used to study other thought-provoking problems.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 155 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:219466 CAPLUS <<LOGINID::20100206>>
DN 137:18119
TI Gene expression profiling identifies significant differences between the molecular phenotypes of bone marrow-derived and circulating human CD34+ hematopoietic stem cells
AU Steidl, Ulrich; Kronenwett, Ralf; Rohr, Ulrich-Peter; Fenk, Roland; Kliszewski, Slawomir; Maercker, Christian; Neubert, Peter; Aivado, Manuel; Koch, Judith; Modlich, Olga; Bojar, Hans; Gattermann, Norbert; Haas, Rainer
CS Department of Hematology, Oncology and Clinical Immunology, University of Dusseldorf, Dusseldorf, D-40225, Germany
SO Blood (2002), 99(6), 2037-2044 CODEN: BLOOAW; ISSN: 0006-4971
PB American Society of Hematology
DT Journal
LA English
AB CD34+ hematopoietic stem cells are used clin. to support cytotoxic therapy, and recent studies raised hope that they could even serve as a cellular source for nonhematopoietic tissue engineering. Here, we examd. in 18 volunteers the gene expressions of 1185 genes in highly enriched bone marrow CD34+ (BM-CD34+) or granulocyte-colony-stimulating factor-mobilized peripheral blood CD34+ (PB-CD34+) cells by means of cDNA array technol. to identify mol. causes underlying the functional differences between circulating and sedentary hematopoietic stem and progenitor cells. In total, 65 genes were significantly differentially expressed. Greater cell cycle and DNA synthesis activity of BM-CD34+ than PB-CD34+ cells were reflected by the 2- to 5-fold higher expression of 9 genes involved in cell cycle progression, 11 genes regulating DNA synthesis, and cell cycle-initiating transcription factor E2F-1. Conversely, 9 other transcription factors, including the differentiation blocking GATA2 and N-myc, were expressed 2 to 3 times higher in PB-CD34+ cells than in BM-CD34+ cells. Expression of 5 apoptosis driving genes was also 2 to 3 times greater in PB-CD34+ cells, reflecting a higher apoptotic activity. In summary, our study provides a gene expression profile of primary human CD34+ hematopoietic cells of the blood and marrow. Our data molecularly confirm and explain the finding that CD34+ cells residing in the bone marrow cycle more rapidly, whereas circulating CD34+ cells consist of a higher no. of quiescent stem and progenitor cells. Moreover, our data provide novel mol. insight into stem cell physiol.
OSC.G 74 THERE ARE 74 CAPLUS RECORDS THAT CITE THIS RECORD (74 CITINGS)
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 156 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:198129 CAPLUS <<LOGINID::20100206>>
DN 136:243356
TI Structural genomics, proteomics, and SNPs
AU Ishiguro, Masaji
CS Suntory Inst. Bioorg. Res., Japan
SO Farumashia (2002), 38(2), 125-129 CODEN: FARUAW; ISSN: 0014-8601
PB Pharmaceutical Society of Japan
DT Journal; General Review
LA Japanese
AB A review on ligand-receptor interactions, relations between SNPs (single nucleotide polymorphysms) and protein conformation ***changes*** , and ***proteomics*** , from the point of view of ***drug*** discovery.

L12 ANSWER 157 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:181842 CAPLUS <<LOGINID::20100206>>
DN 137:3400
TI Drosophila melanogaster myotropins have unique functions and signaling pathways
AU Merte, J.; Nichols, R.
CS Department of Biological Chemistry, University of Michigan, Ann Arbor, MI, 48109-1048, USA
SO Peptides (New York, NY, United States) (2002), 23(4), 757-763 CODEN: PPTDD5; ISSN: 0196-9781
PB Elsevier Science Inc.
DT Journal
LA English
AB Drosophila melanogaster TDVDHVFLRFamide (DMS), SDNFMRFamide, and pEVRFRQCYFNPISCF (FLT) represent three structurally distinct peptide families. Each peptide decreases heart rate albeit with different magnitudes and time-dependent responses. DMS and FLT are expressed in the crop and decrease crop motility; however, SDNFMRFamide expression and effect on the crop has not been reported. These data suggest the peptides have different physiol. roles. The peptides have non-overlapping expression patterns in neural tissue, which suggests different mechanisms regulate their synthesis and release. The structures, ***expression*** ***patterns*** , and ***activities*** of the myotropins suggest they have important but ***different*** roles in biol. and different signaling pathways.

OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 158 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:152676 CAPLUS <<LOGINID::20100206>>
DN 138:53031
TI Genes, telomeres and mammalian aging
AU Goyns, Malcolm H.
CS Molecular Gerontology Unit, School of Sciences, University of Sunderland, Sunderland, SR1 3SD, UK
SO Mechanisms of Ageing and Development (2002), 123(7), 791-799 CODEN: MAGDA3; ISSN: 0047-6374
PB Elsevier Science Ireland Ltd.
DT Journal; General Review
LA English
AB A review. Although there appear to be several influences, which contribute to the aging of mammals, the role of DNA appears to be pivotal. There is increasing evidence that oxidative damage is an important factor in producing mutations in genes, shortening telomeres, and damaging mitochondrial DNA. Accumulation of mutations in genomic DNA could result in the gradual decline in cellular function, which is exhibited in a variety of tissues. The random nature of these mutations, could also offer an explanation for differences in the degree and time of onset of age-related changes, exhibited by different individuals. Shortening of telomeres, caused by oxidative damage or the end-replication problem, could result in the accumulation of post-mitotic cells in-vivo during ageing. This might impair certain aspects of physiol., such as wound healing. Mutation of mitochondrial DNA may also be important in causing loss of cells in post-mitotic tissues such as muscle or brain. In addn. changes in the redox state during the life of an animal may alter transcription factor ***activities*** , leading to consistent ***changes*** in the gene ***expression*** ***profiles*** of mammalian tissues. The latter could explain consistent age-related changes that have been obsd. in cell structure and physiol. Although all of these mechanisms may make a contribution to aging, it is likely that it is the interplay between them that produces the most prominent effects.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 86 THERE ARE 86 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 159 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:122704 CAPLUS <<LOGINID::20100206>>
DN 136:162380
TI Protein and cDNA sequences of human GTPase activating protein negative regulator-like protein and therapeutic uses thereof
IN Mao, Yumin; Xie, Yi
PA Biowindow Gene Development Inc., Peop. Rep. China
SO PCT Int. Appl., 37 pp. CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 2002011511 A1 20020214 WO 2001-CN1008 20010619
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CZ, CH, CO, CR, CU, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
CN 1329024 A 20020102 CN 2000-116684 20000621
AU 2001093636 A 20020214 AU 2001-93636 20010619
PRAI CN 2000-116684 A 20000621
WO 2001-CN1008 W 20010619
AB The invention provides protein and cDNA sequences of a novel human protein with the mol. wt. of 11.66 kDa from fetus brain, which has similar ***expression*** ***pattern*** as human GTPase ***activating*** protein neg. regulator in ***different*** human tissues and cell lines. The invention also relates to constructing GTPase activating protein neg. regulator-like protein expression vectors to prep. recombinant protein using prokaryote or eukaryote cells. It also disclosed the method of applying the protein for the treatment of various kinds of diseases, such as cancer, hemopathy, development disease, HIV infection, immune disease and inflammation. The antagonist of the protein and its therapeutic uses are also disclosed.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 160 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:119171 CAPLUS <<LOGINID::20100206>>
DN 137:183823
TI Antioxidant agents have a different expression pattern in muscle fibers of patients with mitochondrial diseases
AU Filosto, Massimiliano; Tonin, Paola; Vattemi, Gaetano; Spagnolo, Michele; Rizzuto, Nicolo; Tomelleri, Giuliano
CS Section of Clinical Neurology, Department of Neurological Sciences and Vision, University of Verona, Policlinico G.B. Rossi, Verona, 37134, Italy
SO Acta Neuropathologica (2002), 103(3), 215-220 CODEN: ANPTAL; ISSN: 0001-6322
PB Springer-Verlag
DT Journal
LA English
AB Respiratory chain dysfunction leads to reactive oxygen species (ROS) generation with following oxidative stress and cellular damage. A histochem. and immunohistochem. study was performed on muscle biopsies from 17 patients with mitochondrial disease [chronic progressive external ophthalmoplegia (CPEO), mitochondrial encephalomyopathy with lactic acidosis and stroke-like episodes (MELAS), myoclonic epilepsy with ragged red fibers (MERRF)] to evaluate the expression pattern and location of manganese superoxide dismutase (MnSOD), copper-zinc superoxide dismutase (CuZnSOD) and reduced glutathione (GSH) in skeletal muscle fibers. Our data showed that: (1) MnSOD, CuZnSOD and GSH are expressed in fibers with respiratory chain deficiency; (2) the antioxidant induction is correlated with the degree of mitochondrial proliferation, but not with clin. phenotype, patients' age, duration of disease, biochem. defects or mitochondrial DNA abnormalities. In addn., we suggest that expression of MnSOD and GSH may be considered an initial, indirect sign of respiratory chain dysfunction because it is obsd. in the early stages of the disease.

OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 161 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:74935 CAPLUS <<LOGINID::20100206>>
DN 137:163206
TI Using mRNA expression profiling to determine anticancer drug efficacy
AU Los, Gerrit; Yang, Fei; Samimi, Goli; Manorek, Gerald; Guerorguieva, Ivelina M.; Howell, Stephan; van Erp, Nielka; Breaux, James K.
CS UCSD Cancer Center, University of California at San Diego, La Jolla, CA, 92037-0058, USA
SO Cytometry (2002), 47(1), 66-71 CODEN: CYTODQ; ISSN: 0196-4763
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Pharmacogenomics is a fast-growing field of investigations that aims to further elucidate the inherited nature of inter-individual differences in drug disposition and effects, with the ultimate goal of providing a stronger scientific basis for selecting the optimal drug therapy. Providing the right drug for the right patient is an important problem in the treatment of cancer. This is mainly due to the lack of information about the sensitivity of the tumor for a specific treatment modality, such as either chemotherapy or radiation treatment. This presentation highlights two approaches to identify responsiveness to treatment. Both approaches are based on the identification of expression profiles. The first approach concs. on drug resistance and the second on the signaling pathways leading up to the death of the cell. Both approaches provide expression profiles; however, the more dynamic expression profiling as used to det. the signaling in damage cells promises to be a better determinant for the pharmacogenomic ***changes*** in ***expression*** ***profiles*** and, consequently, a potential better determinant for ***drug*** efficacy.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 162 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:30197 CAPLUS <<LOGINID::20100206>>
DN 136:194416
TI The activin binding proteins follistatin and follistatin-related protein are differentially regulated in vitro and during cutaneous wound repair
AU Wankell, M.; Kaesler, S.; Zhang, Y-Q.; Florence, C.; Werner, S.; Duan, R.
CS Institute of Cell Biology, ETH Zurich, Zurich, CH-8093, Switz.
SO Journal of Endocrinology (2001), 171(3), 385-395 CODEN: JOENAK; ISSN: 0022-0795
PB Society for Endocrinology
DT Journal
LA English
AB Follistatin is a secreted protein that binds activin in vitro and in vivo and thereby inhibits its biol. functions. Recently, related human and murine genes, designated follistatin-related gene (FLRG), were identified, and their products were shown to bind activin with high affinity. In this study we further characterized the murine FLRG protein, and we analyzed its tissue-specific expression and regulation in comparison with those of follistatin. Transient expression of the mouse FLRG protein in COS-1 cells revealed that the FLRG cDNA encodes a secreted glycoprotein. FLRG mRNA was expressed at high levels in the lung, the testis, the uterus and, particularly, the skin. Immunohistochem. revealed the presence of FLRG in the basement membrane between the dermis and the epidermis and around blood vessels. FLRG mRNA expression was induced in keratinocytes by keratinocyte growth factor, epidermal growth factor and transforming growth factor-.beta.1, and in fibroblasts by platelet-derived growth factor and epidermal growth factor. The induction was more rapid, but weaker, than that of follistatin. Most interestingly, both follistatin and FLRG were expressed during the wound healing process, but their distribution within the wound was different. The different ***expression*** ***pattern*** of FLRG and follistatin and their ***differential*** regulation suggest ***different*** functions of these ***activin*** -binding proteins in vivo.
OSC.G 23 THERE ARE 23 CAPLUS RECORDS THAT CITE THIS RECORD (23 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 163 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:16934 CAPLUS <<LOGINID::20100206>>
DN 136:399575
TI Phosphorylation of the serine 60 residue within the Cdx2 activation domain mediates its transactivation capacity
AU Rings, Edmond H. H. M.; Boudreau, Francois; Taylor, Jennifer K.; Moffett, Jennifer; Suh, Eun Ran; Traber, Peter G.
CS Division of Gastroenterology, Department of Medicine, University of Pennsylvania, Philadelphia, PA, USA
SO Gastroenterology (2001), 121(6), 1437-1450 CODEN: GASTAB; ISSN: 0016-5085
PB W. B. Saunders Co.
DT Journal
LA English
AB Cdx2 is crit. in intestinal proliferation and differentiation. Modulation of Cdx2 function in response to cellular signaling is to be elucidated. The authors hypothesize that phosphorylation of the Cdx2 activation domain can modulate its function. The Cdx2 activation domain was delineated in transient transfections using different portions of Cdx2 fused to the Gal4-DNA binding domain. In vivo phosphorylation was studied by metabolic labeling with 32P-orthophosphate. To study a potential phosphorylation site, polyclonal antibodies were generated: CNL was raised against amino acids 54-66 of Cdx2 and P-Cdx2-S60 against the same epitope in which serine 60 was phosphorylated. A crit. region for transactivation resides within amino acids 60-70. Substitution of serine 60 with alanine reduces incorporation of 32P-orthophosphate substantially. S60-phosphorylation decreases Cdx2 transactivation. Phosphorylation of serine 60 can be inhibited with the mitogen-activated protein kinase inhibitors PD98059 or U0126. P-Cdx2-S60 recognizes phosphorylated serine 60 mainly in proliferative compartment of the intestinal epithelial layer. In contrast, CNL recognizes Cdx2 predominantly in the differentiated compartment. Thus, the Cdx2 activation domain is phosphorylated at serine 60 via the mitogen-activated protein kinase pathway. S60-phosphorylated and S60-nonphosphorylated Cdx2 have ***different*** transcriptional ***activity*** , as well as ***different*** spatial

expression ***patterns*** in the intestinal epithelium.
OSC.G 40 THERE ARE 40 CAPLUS RECORDS THAT CITE THIS RECORD (40 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 164 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:930062 CAPLUS <<LOGINID::20100206>>
DN 137:89296
TI A gene expression profile of embryonic stem cells and embryonic stem cell-derived neurons
AU Loring, J. F.; Porter, J. G.; Seilhamer, J.; Kaser, M. R.; Wesselschmidt, R.
CS Department of Life Sciences, Incyte Genomics, Inc., Palo Alto, CA, 94304, USA
SO Restorative Neurology and Neuroscience (2001), 18(2,3), 81-88 CODEN: RNNEEL; ISSN: 0922-6028
PB IOS Press
DT Journal
LA English
AB Embryonic stem (ES) cells have the ability to differentiate into a variety of cell lineages. We are examg. ES cell differentiation in vitro by using cDNA microarrays to generate a mol. phenotype for each cell type. E14 ES cells induced by retinoic acid after forming embryoid bodies differentiate almost exclusively to neurons. We obtained expression patterns for about 8500 gene sequences by comparing mRNAs from undifferentiated ES cells and their differentiated derivs. in a competitive hybridization. Our results indicate that the genes expressed by ES cells change dramatically as they differentiate (58 gene sequences up-regulated, 34 down-regulated). Most notably, totipotent ES cells expressed high levels of a repressor of Hox expression (the polycomb homolog Mph1) and a co-repressor (CTBP2). Expression of these genes was undetectable in differentiated cells; the ES cell-derived neurons expressed a different set of transcriptional regulators, as well as markers of neurogenesis. The gene ***expression*** ***profiles*** indicate that ES cells ***actively*** suppress ***differentiation*** by transcriptional repression; cell-cell contact in embryoid bodies and retinoic acid treatment may overcome this suppression, allowing expression of Hox genes and inducing a suite of neuronal genes. Gene expression profiles will be a useful outcome measure for comparing in vitro treatments of differentiating ES cells and other stem cells. Also, knowing the mol. phenotype of transplantable cells will allow correlation of phenotype with the success of the transplant.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 165 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:925064 CAPLUS <<LOGINID::20100206>>
DN 136:381158
TI Gene expression profiling of low selenium status in the mouse intestine: transcriptional activation of genes linked to DNA damage, cell cycle control and oxidative stress
AU Rao, Lin; Puschner, Birgit; Prolla, Tomas A.
CS Departments of Genetics and Medical Genetics, University of Wisconsin-Madison, Madison, WI, 53706, USA
SO Journal of Nutrition (2001), 131(12), 3175-3181 CODEN: JONUAI; ISSN: 0022-3166
PB American Society for Nutritional Sciences
DT Journal
LA English
AB The essential trace mineral selenium (Se) has been shown previously to inhibit intestinal, prostate, lung and liver tumor development and assocd. mortality in both exptl. animals and humans. Although Se is likely to be one of the most powerful cancer chemopreventive agents in the human diet, its mechanism of action is unknown. To better understand the biol. consequences of alterations in Se status, the gene expression profile assocd. with low Se status in the intestine of C57Bl/6J mice was analyzed. Mice were fed either a high fat (14%), torula yeast-based, Se-deficient diet (<0.01 mg/kg) or the same diet supplemented with a high level of dietary Se (1 mg/kg, as seleno-L-methionine) for 90 d. Use of high d. oligonucleotide arrays representing 6347 genes revealed that low Se status results in a ***differential*** gene ***expression*** ***pattern*** indicative of ***activation*** of genes involved in DNA damage, oxidative stress and cell cycle control, and a decrease in the expression of genes involved in detoxification. These results suggest that suboptimal intake of a single trace mineral can have broad effects on gene expression patterns, providing a framework for understanding the multiple beneficial effects of Se in cancer chemoprevention and human health.
OSC.G 43 THERE ARE 43 CAPLUS RECORDS THAT CITE THIS RECORD (43 CITINGS)
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 166 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:920864 CAPLUS <<LOGINID::20100206>>
DN 136:384813
TI Analysis of the in vivo dendritic cell response to the bacterial superantigen staphylococcal enterotoxin B in the mouse spleen
AU Yoon, S.; Bae, K. L.; Shin, J. Y.; Yoo, H. J.; Lee, H. W.; Baek, S. Y.; Kim, B. S.; Kim, J. B.; Lee, H. D.
CS Department of Anatomy, College of Medicine, Pusan National University, Pusan, 602-739, S. Korea
SO Histology and Histopathology (2001), 16(4), 1149-1159 CODEN: HIHIES; ISSN: 0213-3911
PB Histology and Histopathology
DT Journal
LA English
AB To investigate the in vivo effects of Staphylococcal enterotoxin B (SEB) on dendritic cells (DCs) in the spleen, a single dose of SEB (50 .mu.g/kg) was administered to BALB/c mice by i.p. injection. Afterwards, the mice were sacrificed at 2, 6 and 24 h, 2, 4, 7 and 15 days, and the spleens were removed. The immunocytochem. characterization of the cells was carried out using various monoclonal antibodies in cryostat-cut sections. The distribution patterns of DCs and their major costimulatory mols., CD80, CD86 and CD40 in the spleen were identified, and the evidence for maturation of DCs in vivo in response to SEB was obtained. It was found that systemic administration of SEB induced the migration of most of the immature, splenic DCs from the marginal zone to the periarterial lymphatic sheath within 6 h. This movement paralleled a maturation process, as assessed by upregulation of CD40, CD80 and CD86 expression in the interdigitating dendritic cells (IDCs). The upregulation of costimulatory mol. expression was conspicuous only in DCs in contrast to other antigen-presenting cells (APCs) such as

macrophages and B cells which did not show any significant alterations in their costimulatory mol. expression. We also demonstrated the temporal expression pattern of these costimulatory mols. on the activated DCs. The upregulation of costimulatory mols. on DCs reached a peak level 6 h after SEB injection, while the increase in no. of T cells expressing T cell receptor V.beta.8 reached a peak level on day 2 after SEB treatment. In conclusion, we demonstrated the in vivo DC response to SEB in the mouse spleen, esp. a potent stimulative effect of SEB on DCs in vivo, a temporal distribution pattern of DCs as well as T cells including TCR V.beta.8+ T cells, and a ***differential*** ***expression*** ***pattern*** of costimulatory mols. on the ***activated*** DCs. The results of the present study indicate that DCs are the principal type of APCs which mediate T cell activation by SAg in vivo, and that each costimulatory mol. may have different role in the activation of DCs by SAg. Thus, it is plausible to speculate that DCs play a crit. role in the T cell clonal expansion by SAgs and other SAg-induced immune responses in vivo.
CSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 167 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:873907 CAPLUS <<LOGINID::20100206>>
DN 137:58038
TI Prospect of expression profiling of pathogenic genes using microarrays
AU Yang, Xing; Mao, Xiao-Quan; On, Adra; Otsu, Akiko; Shirakawa, Taro
CS Beth Israel Research Institute, Harvard University, USA
SO Arerugi, Men'eki (2001), 8(10), 1108-1112 CODEN: ARMEFS; ISSN: 1344-6932
PB Iyaku Janarusha
DT Journal; General Review
LA Japanese
AB A review gives a tech. overview of DNA microarray anal. This paper also discussed the application of the microarray technologies to the approaches for identifying the genes responsible for diseases and mining novel ***drug*** targets by analyzing the ***differences*** in the gene ***expression*** ***profiles*** and the genetic polymorphisms between healthful and sick subjects.

L12 ANSWER 168 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:872679 CAPLUS <<LOGINID::20100206>>
DN 136:67607
TI Stage- and tissue-specific expression of a .beta.-1,4-galactosyltransferase in the embryonic epidermis
AU Uehara, Kazuyoshi; Thelu, Jacques
CS Biologie de la Differenciation Epithéliale, Universite Joseph Fourier, Tronche, 38706, Fr.
SO In Vitro Cellular & Developmental Biology: Animal (2001), 37(9), 613-617 CODEN: IVCAED; ISSN: 1071-2690
PB Society for In Vitro Biology
DT Journal
LA English
AB Changes in oligosaccharide structures of glycoconjugates have been obsd., and are postulated to play key roles in embryonic development and differentiation. N-Acetylglucosamine (GlcNAc) .beta.-1,4-galactosyltransferase AKI (I) showed ***different*** ***expression*** ***patterns*** in time and space, and ***different*** enzymic ***activity*** from the other known family members. The epidermis of mouse embryo included a high level of I activities, which transferred galactose (Gal) to endogenous glycoprotein (mol. wt., 130 kDa) (GP130). The max. activity was for 13.5-day postcoitum embryos. Specific antibody against I inhibited 81% of I activities, which indicates that I represents the major part of the embryonic epidermis enzymes. I shows 2.2-fold higher galactosyltransferase activity toward Gal-acceptor glucose with .alpha.-lactalbumin (.alpha.-LA) than toward GlcNAc without .alpha.-LA. I was also expressed in mouse melanoma and leukemia cell lines and in human basal cell carcinoma specimens. The GP130 Gal acceptor once galactosylated by I may be directly involved in epidermal differentiation and oncogenesis.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 169 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:866334 CAPLUS <<LOGINID::20100206>>
DN 136:197469
TI Expression of HNF4.alpha. isoforms in mouse liver development is regulated by sequential promoter usage and constitutive 3' end splicing
AU Torres-Padilla, Maria Elena; Fougere-Deschatrette, Catherine; Weiss, Mary C.
CS Unite de Genetique de la Differenciation, Departement de Biologie Moleculaire, FRE 2364 du CNRS, Institut Pasteur, Paris, Fr.
SO Mechanisms of Development (2001), 109(2), 183-193 CODEN: MEDVE6; ISSN: 0925-4773
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Hepatocyte nuclear factor 4.alpha. (HNF4.alpha.) is essential for the establishment and maintenance of liver-specific gene expression. The HNF4.alpha. gene codes for several isoforms whose developmental and physiol. relevance has not yet been explored. HNF4.alpha.1 and HNF4.alpha.7 originate from different promoters, while alternative splicing in 3' leads to HNF4.alpha.2 and HNF4.alpha.8, resp. HNF4.alpha.7/.alpha.8 were abundantly expressed in embryonic liver and fetal-like hepatoma cells. HNF4.alpha.1/.alpha.2 transcripts were up-regulated at birth and represented the only isoforms in adult-like hepatoma cells. In line with its expression profile, HNF4.alpha.7 activated more avidly than HNF4.alpha.1 reporter plasmids for genes that are expressed early. The ***expression*** ***patterns*** of both isoforms together with the ***differences*** obsd. in their transcriptional ***activities*** provide elements accounting for fine-tuning of the activity of HNF4.alpha.. The sequential expression of HNF4.alpha.7/.alpha.8 and HNF4.alpha.1/.alpha.2 during mouse liver development is the only modification in liver-enriched transcription factors thus far recorded, which parallels the transition from the fetal to the adult hepatic phenotype.
OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 170 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2001:803279 CAPLUS <<LOGINID::20100206>>
DN 136:17380
TI Proteomics of breast cancer for marker discovery and signal pathway profiling
AU Hondermarck, Hubert; Vercoutter-Edouart, Anne-Sophie; Revillion, Francoise; Lemoine, Jerome; El-Yazidi-Belkoura, Ikram; Nurcombe, Victor; Peyrat, Jean-Philippe
CS Laboratoire de Biologie du Developpement UPRES-EA 1033, Universite des Sciences et Technologies de Lille, Villeneuve d'Ascq, 59650, Fr.
SO Proteomics (2001), 1(10), 1216-1232 Published in: Electrophoresis, 22(18) CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH
DT Journal; General Review
LA English
AB A review. Breast cancer is the most common form of cancer among women and the identification of markers to discriminate tumorigenic from normal cells, as well as the different stages of this pathol., is of crit. importance. Two-dimensional electrophoresis has been used before for studying breast cancer, but the progressive completion of human genomic sequencing and the introduction of mass spectrometry, combined with advanced bioinformatics for protein identification, have considerably increased the possibilities for characterizing new markers and therapeutic targets. Breast cancer proteomics has already identified markers of potential clin. interest (such as the mol. chaperone 14-3-3 sigma) and technol. innovations such as large scale and high throughput anal. are now driving the field. Methods in functional proteomics have also been developed to study the intracellular signaling pathways that underlie the development of breast cancer. As illustrated with fibroblast growth factor-2, a mitogen and mitogen factor for breast cancer cells, proteomics is a powerful approach to identify signaling proteins and to decipher the complex signaling circuitry involved in tumor growth. Together with genomics, ***proteomics*** is well on the way to molecularly characterizing the ***different*** types of breast tumor, and thus defining new ***therapeutic*** targets for future treatment.
OSC.G 68 THERE ARE 68 CAPLUS RECORDS THAT CITE THIS RECORD (68 CITINGS)
RE.CNT 88 THERE ARE 88 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 171 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:799980 CAPLUS <<LOGINID::20100206>>
DN 136:128850
TI The characterization of PPAR.alpha. ligand ***drug*** action in an in vivo model by comprehensive ***differential*** gene ***expression*** ***profiling***
AU Rothberg, Bonnie E. Gould; Sundseth, Scott S.; DiPippo, Vincent A.; Brown, Peter J.; Winegar, Deborah A.; Gottshalk, William K.; Shenoy, Suresh G.; Rothberg, Jonathan M.
CS CuraGen Corporation, New Haven, CT, 06511, USA
SO Functional & Integrative Genomics (2001), 1(5), 294-304 CODEN: FIGUBY; ISSN: 1438-793X
PB Springer-Verlag
DT Journal
LA English
AB Expression pharmacogenomics includes differential gene expression (DGE) profiling of drug responses in model systems to generate a set of differentially modulated drug-responsive genes which can serve as a surrogate measure for drug action. In this manner, expression pharmacogenomics bridges the fields of genomics and medicinal chem. Addnl., modulated genes can be organized into metabolic and signaling pathways that highlight the mechanism of drug activity in a selected tissue. Here, we describe the application of expression pharmacogenomics to characterize a drug response in the clin. relevant in vivo model, the Sprague-Dawley rat. Following oral dosing of rats with GW9578, a novel synthetic peroxisome proliferator activated receptor alpha (PPAR.alpha.) ligand indicated for lipid disorders, we applied Gene-Calling, a differential mRNA transcript profiling technique, to rat liver cDNA. Following GW9578 treatment, 2.4% of the rat liver genes were differentially expressed. We confirmed the sequence identity of 50 distinctly modulated genes. DGE was obsd. among genes representative of at least six discrete metabolic pathways. Furthermore, we obsd. up-regulation of 20 genes involved in mitochondrial, peroxisomal and microsomal fatty acid oxidn., consistent with mol. biol. and clin. data indicating PPAR.alpha. ligand principal efficacy to be through increasing fatty acid metab. Those pathways regulated in our study that are potentially contributory to target effect, non-target adverse effects, or of unknown consequence include xenobiotic detoxification and steroid modification. Finally, comprehensive drug response profiling can lead to the serendipitous discovery of novel disease indications. In this case, these results suggest a potential novel indication for GW9578 in the treatment of X-linked adrenoleukodystrophy. We have shown, therefore, that the organization of DGE results into metabolic and signaling pathways can elucidate mechanisms of pharmacol. desired (i.e., efficacious) and, where appropriate, undesired (i.e., potentially deleterious) effects.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 172 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:766236 CAPLUS <<LOGINID::20100206>>
DN 136:115958
TI Proteome Survey of Proliferating and Differentiating Rat RPE-J Cells
AU West, Karen A.; Yan, Lin; Miyagi, Masaru; Crabb, John S.; Marmorstein, Alan D.; Marmorstein, Lihua; Crabb, John W.
CS Cole Eye Institute, Lerner Research Institute, Cleveland Clinic Foundation, Cleveland, OH, 44195, USA
SO Experimental Eye Research (2001), 73(4), 479-491 CODEN: EXERA6; ISSN: 0014-4835
PB Academic Press
DT Journal
LA English
AB The suitability of the rat derived SV-40T immortalized RPE-J cell line for identifying proteome changes assocd. with RPE differentiation was evaluated by surveying changes in protein expression levels. Rat RPE-J cells were induced to undergo differentiation in culture by growth at the nonpermissive temp. of 40.degree. in the presence of retinoic acid. Total proteins were extd. from cells grown under proliferating or differentiating conditions and sepd. by 1D and 2D gel electrophoresis. Gel spots were excised, digested in situ with trypsin, and analyzed by mass spectrometry to identify proteins. Computer assisted image anal. was used to align gel patterns and quantify spot intensities. Neither proliferating nor differentiating RPE-J cell cultures exhibited detectable levels of cellular retinaldehyde-binding protein, RPE65, 11-cis-retinol dehydrogenase or lecithin retinol acyl transferase, suggesting that RPE-J cells are not appropriate for visual cycle studies. About 18% of the 61 identified proteins appear to change expression levels with the cell growth

conditions. Seven proteins appeared to be up-regulated and four proteins down-regulated when the cells were changed from proliferating to differentiating culture conditions. The majority of the apparent changes in protein expression levels were assocd. with stress response genes. Significant changes in the apparent mass and charge properties of proteins were also obsd. and for select proteins, the modifications appeared to be correlated with cell growth conditions. The results demonstrate that proteome differences in RPE-J cells assocd. with growth conditions can be identified and support the suitability of RPE-J cells for more targeted and/or more global proteome anal. of RPE differentiation. (c) 2001 Academic Press.
OSC.G 29 THERE ARE 29 CAPLUS RECORDS THAT CITE THIS RECORD (29 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 173 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:764650 CAPLUS <<LOGINID::20100206>>
DN 136:146310
TI Oxygen-dependent expression of hypoxia-inducible factor 1.alpha. in renal medullary cells rats
AU Zou, Ai-Ping; Yang, Zhi-Zhang; Li, Pin-Lan; Cowley, Allen W., Jr.
CS Dep. Physiol. and Pharmacol. and Toxicology, Medical Coll. of Wisconsin, Milwaukee, WI, 53226, USA
SO Physiological Genomics [online computer file] (2001), 6(3), 159-168 CODEN: PHGEFP; ISSN: 1094-8341 URL: http://physiolgenomics.physiology.org/cgi/reprint/6/3/159.pdf
PB American Physiological Society
DT Journal; (online computer file)
LA English
AB Hypoxia-inducible factor-1.alpha. (HIF-1.alpha.) is a transcription factor that regulates the oxygen-dependent expression of a no. of genes. This transcription factor may contribute to the abundant expression of many genes in renal medullary cells that function normally under hypoxic conditions. The present study was designed to det. the characteristics of HIF-1.alpha. cDNA cloned from the rat kidney and the ***expression*** ***profile*** of HIF-1.alpha. in ***different*** kidney regions and to explore the mechanism ***activating*** or regulating HIF-1.alpha. expression in renal medullary cells. A3,718-bp HIF-1.alpha. cDNA from the rat kidney was first cloned and sequenced using RT-PCR and TA cloning technique. It was found that 823 amino acids deduced from this renal HIF-1.alpha. cDNA had 99%, 96%, and 90% identity with rat, mouse, or human HIF-1.alpha. deposited in GenBank, resp. The 3'-untranslated region of HIF-1.alpha. mRNA from the rat kidney contained seven AUUUA instability elements, five of which were found to be conserved among rat, mouse, and human HIF-1.alpha.. Northern blot analyses demonstrated a corticomedullary gradient of HIF-1.alpha. mRNA expression in the kidney, with the greatest abundance in the renal inner medulla. Western blot analyses also detected a higher HIF-1.alpha. protein level in the nuclear exts. from the renal medulla than the renal cortex. A classic loop diuretic, furosemide (10 mg/kg i.p.), markedly increased renal medullary PO2 levels from 22.5 to 52.2 mmHg, which was accompanied by a significant redn. of HIF-1.alpha. transcripts in renal medullary tissue. In in vitro expts., low PO2, but not elevated osmolarity, was found to significantly increase HIF-1.alpha. mRNA in renal medullary interstitial cells and inner medullary collecting duct cells. These results indicate that HIF-1.alpha. is more abundantly expressed in the renal medulla compared with the renal cortex. Increased abundance of HIF-1.alpha. mRNA in the renal medulla may represent an adaptive response of renal medullary cells to low PO2.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 174 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:697273 CAPLUS <<LOGINID::20100206>>
DN 136:148347
TI High-density DNA microarray membranes to study gene expression patterns associated with human airway epithelial cell differentiation in culture
AU Chang, Mary M. J.; Chen, Yin; Zhao, Yu Hua; Wu, Reen; Li, Ching; Peck, Konan
CS University of California, Davis, CA, USA
SO Cilia and Mucus: From Development to Respiratory Defense, [International Meeting], 2nd, Sirmione, Italy, Nov. 3-4, 1999 (2001), Meeting Date 1999, 225-237. Editor(s): Salathe, Matthias. Publisher: Marcel Dekker, Inc., New York, N. Y. CODEN: 69BVC5
DT Conference
LA English
AB The purpose of this paper is to utilize the newly developed technol. of microarray membranes to analyze genes whose expression is assocd. with mucociliary differentiation of human airway epithelial cells in vivo. Two types of nylon membranes were used. One contains 884 sequence-verified expression sequence tag (EST) clones, the other contains 576-uni EST clones. Data obtained from these membranes were further characterized by Northern blot hybridization.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 175 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:691194 CAPLUS <<LOGINID::20100206>>
DN 135:369962
TI Variable .beta.-catenin expression in colorectal cancers indicates tumor progression driven by the tumor environment
AU Brabletz, Thomas; Jung, Andreas; Reu, Simone; Porzner, Marc; Hlubek, Falk; Kunz-Schughart, Leoni A.; Knuechel, Ruth; Kirchner, Thomas
CS Department of Pathology, University of Erlangen-Nurnberg, Erlangen, 91054, Germany
SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(18), 10356-10361 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Invasion and dissemination of well-differentiated carcinomas are often assocd. with loss of epithelial differentiation and gain of mesenchyme-like capabilities of the tumor cells at the invasive front. However, when comparing central areas of primary colorectal carcinomas and corresponding metastases, we again found the same differentiated epithelial growth patterns. These characteristic phenotypic changes were assocd. with distinct expression patterns of .beta.-catenin, the main oncogenic protein in colorectal carcinomas, and E-cadherin. Nuclear .beta.-catenin was found in dedifferentiated mesenchyme-like tumor cells at the invasive front, but strikingly, as in central areas of the primary tumors, was localized to the membrane and cytoplasm in

polarized epithelial tumor cells in the metastases. This ***expression*** ***pattern*** was accompanied by ***changes*** in E-cadherin expression and proliferative ***activity***. On the basis of these data, we postulate that an important driving force for progression of well-differentiated colorectal carcinomas is the specific environment, initiating two transient phenotypic transition processes by modulating intracellular .beta.-catenin distribution in tumor cells.
OSC.G 196 THERE ARE 196 CAPLUS RECORDS THAT CITE THIS RECORD (196 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 176 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:689431 CAPLUS <<LOGINID::20100206>>
DN 135:355732
TI Proteomic characterization of early-stage differentiation of mouse embryonic stem cells into neural cells induced by all-trans retinoic acid in vitro
AU Guo, Xiaoxia; Ying, Wantao; Wan, Jinghong; Hu, Zhiyuan; Qian, Xiaohong; Zhang, Hongwei; He, Fuchu
CS Department of Genomics and Proteomics, Beijing Institute of Radiation Medicine, Beijing, 100850, Peop. Rep. China
SO Electrophoresis (2001), 22(14), 3067-3075 CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
AB Embryonic stem (ES) cells are totipotent stem cells, which can differentiate into various kinds of cell types, including neurons. They are widely used as a model system for investigating mechanisms of differentiation events during early mouse development. In this study, proteomic techniques were used to approach the protein profile associd. with the early-stage differentiation of ES cells into neuronal cells induced by all-trans retinoic acid (ATRA) in vitro. In comparison of the protein profile of parent ES cells with that of ES-derived neural-committed cells, which was induced by ATRA for four days, 24 differentially displayed protein spots were selected from two-dimensional electrophoresis (2-DE) gels for further protein identification by peptide mass fingerprinting (PMF). Nine proteins were known to be involved in the process of neural differentiation and/or neural survival. Of those, .alpha.-3'.alpha.-7 tubulin and vimentin were downregulated, while cytokeratin 8, cytokeratin 18, G1/S-special cyclin D2, follistatin-related protein, NEL-protein, platelet-activating factor acetylhydrolase IB .alpha.-subunit, and thioredoxin peroxidase 2 were upregulated during differentiation of ES cells to neural cells. Addnl., other 12 protein (five upregulated and seven downregulated) spots associd. with ES cell differentiation into neuronal cells were not matched to known proteins so far, implicating that they might be novel proteins. The results above indicated that the mol. mechanisms of differentiation of ES cells to neural cells in vitro might be similar to those of other neural systems in vitro and identified that proteomic anal. is an effective strategy to comprehensively unravel the regulatory network of differentiation.
OSC.G 57 THERE ARE 57 CAPLUS RECORDS THAT CITE THIS RECORD (57 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 177 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:653261 CAPLUS <<LOGINID::20100206>>
DN 135:317172
TI Nonequivalent nuclear location of immunoglobulin alleles in B lymphocytes
AU Skok, Jane A.; Brown, Karen E.; Azuara, Veronique; Caparros, Marie-Laure; Baxter, Jonathan; Takacs, Katalin; Dillon, Niall; Gray, David; Perry, Robert P.; Merkenschlager, Matthias; Fisher, Amanda G.
CS MRC Clinical Sciences Centre, Imperial College School of Medicine, Hammersmith Hospital, London, W12 0NN, UK
SO Nature Immunology (2001), 2(9), 848-854 CODEN: NIAMCZ; ISSN: 1529-2908
PB Nature America Inc.
DT Journal
LA English
AB Individual B lymphocytes normally express Ig proteins derived from single Ig heavy chain (H) and light chain (L) alleles. Allelic exclusion ensures monoallelic expression of Ig genes by each B cell to maintain single receptor specificity. Here we provide evidence that at later stages of B cell development, addnl. mechanisms may contribute to prioritizing expression of single IgH and IgL alleles. Fluorescent in situ hybridization anal. of primary splenic B cells isolated from normal and genetically manipulated mice showed that endogenous IgH, .kappa. and .lambda. alleles localized to ***different*** subnuclear environments after ***activation*** and had ***differential*** ***expression*** ***patterns***. However, this differential recruitment and expression of Ig alleles was not typically seen among transformed B cell lines. These data raise the possibility that epigenetic factors help maintain the monoallelic expression of Ig.
OSC.G 93 THERE ARE 93 CAPLUS RECORDS THAT CITE THIS RECORD (93 CITINGS)
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 178 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:637101 CAPLUS <<LOGINID::20100206>>
TI Redirecting the specific reactivity of a natural product and its application to functional proteomics
AU Tamiya, Junko; Cravatt, Benjamin F.; Sorensen, Erik J.
CS Department of Chemistry and the Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA, 92037, USA
SO Abstracts of Papers, 222nd ACS National Meeting, Chicago, IL, United States, August 26-30, 2001 (2001), BIOL-090 Publisher: American Chemical Society, Washington, D. C. CODEN: 69BUZP
DT Conference; Meeting Abstract
LA English
AB ***Activity*** -based protein profiling aims to create chem. agents to profile ***changes*** in enzyme ***activity*** in complex ***proteomes***. Combining this methodol. with a natural product scaffold, a library of biotinylated analogs of the natural product fumagillin was constructed and tested against complex proteomes. Fumagillin is an angiogenesis inhibitor, which contains an electrophilic spiroepoxide and a hydrophobic side chain. The spiroepoxide covalently modifies the metalloprotease methionine aminopeptidase-2 (MetAp-2). Variation of the side chain to both hydrophobic and hydrophilic moieties redirected this natural product, facilitating the specific labeling of a diverse no. of proteins directly in complex proteomes.

L12 ANSWER 179 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:608614 CAPLUS <<LOGINID::20100206>>
DN 136:181495
TI Gene expression of adrenomedullin, leptin, their receptors and neuropeptide Y in hormone-secreting and non-functioning pituitary adenomas, meningiomas and malignant intracranial tumors in humans
AU Knerr, I.; Schuster, S.; Nomikos, P.; Buchfelder, M.; Dotsch, J.; Schoof, E.; Fahlbusch, R.; Rascher, W.
CS Departments of Paediatrics and Neurosurgery, University of Erlangen-Nuremberg, Nuernberg, D-91054, Germany
SO Neuropathology and Applied Neurobiology (2001), 27(3), 215-222 CODEN: NANEDL; ISSN: 0305-1846
PB Blackwell Science Ltd.
DT Journal
LA English
AB The aim of this study was to assess human intracranial tumors for their gene expression pattern of the vasoactive peptide adrenomedullin (AM), its receptor (AM-R) and leptin, which exerts multiple biol. effects including proliferation and angiogenesis via the leptin receptor (OB-Rb). Gene activity of neuropeptide Y (NPY) was monitored addnl. We investigated whether there was a characteristic gene ***expression*** ***pattern*** of AM and leptin in ***different*** intracranial tumors, depending on their proliferation ***activity*** and biol. behavior. We investigated 35 non-functioning pituitary adenomas (including eight null cell, four silent plurihormonal, 23 silent gonadotroph adenomas), seven somatotropinomas, seven prolactinomas, eight meningiomas, five astrocytomas, two glioblastoma multiformes and unaffected temporal lobe (n=8). Quant. reverse transcriptase-polymerase chain reaction (TaqMan RT-PCR) was performed. AM mRNA was detectable in all tumor specimens. AM/GAPDH (glyceraldehyde-3-phosphate dehydrogenase) ratio was significantly higher in somatotropinomas, as was AM/CD31 ratio in prolactinomas, compared with inactive adenomas (P < 0.05). AM-R mRNA was found in all tumor subgroups in small quantities but, in general, higher in tumors than in temporal lobe tissue, resp. AM-R/CD31 ratio was significantly higher in prolactinomas than in inactive adenomas (P < 0.05). Leptin was detectable in very low quantities in each subgroup. OB-Rb gene expression was found in all tumor subgroups, OB-Rb/GAPDH ratio was highest for meningiomas (P < 0.0001, compared with temporal lobe). NPY mRNA was detectable in temporal lobe in higher quantities than in tumors (P < 0.0001), and almost undetectable in prolactinomas and astrocytomas. Our data demonstrate that AM and AM-R, NPY, as well as leptin and OB-Rb, are expressed in various intracranial tumors in humans but their particular function has to be elucidated further. At present, there is no evidence for a cross-talk on transcriptional level between the peptidergic vasodilative system AM and the putative angiogenic and proliferation affecting factor leptin.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 180 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:590999 CAPLUS <<LOGINID::20100206>>
DN 135:270524
TI Diverse gene expression and function of semaphorins in developing lung: positive and negative regulatory roles of semaphorins in lung branching morphogenesis
AU Kagoshima, Masako; Ito, Takaaki; Kitamura, Hitoshi; Goshima, Yoshio
CS Department of Pharmacology, Yokohama City University School of Medicine, Yokohama, 236-0004, Japan
SO Genes to Cells (2001), 6(6), 559-571 CODEN: GECEFL; ISSN: 1356-9597
PB Blackwell Science Ltd.
DT Journal
LA English
AB Previously, we reported that Sema3A, one of the secreted repulsive axon guidance mols., CRMP (collapsin response mediator protein)-2, a putative intracellular signalling mol. for Sema3A and Sema3A receptor neuropilin-1 are expressed in the developing lung. Sema3A inhibits branching morphogenesis of embryonic lung in organ culture. We examd. the gene expression of Sema3A, Sema3C, Sema3F and their receptors, NP-1, NP-2 and plexin-A1 by in situ hybridization. Transcripts of all six genes were detected in mouse lung from embryonic day E11.5 to E17.5, and displayed highly specific spatiotemporal distributions. The distribution of the receptor genes was detected in patterns which were consistent with known receptor usage of the semaphorins. In contrast to Sema3A, we found that the other class 3 semaphorins, Sema3C and Sema3F, stimulated branching morphogenesis. This stimulatory effect of Sema3C or Sema3F was accompanied by a moderate increase in the incorporation of bromodeoxyuridine (BrdU) into DNA in the terminal epithelial cells. The coordinated ***expression*** ***patterns*** of ***different*** semaphorins and their receptors, together with the specific ***activities*** affecting branching morphogenesis, suggest that the semaphorins act as both pos. and neg. regulators of branching morphogenesis in the developing lung.
OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 181 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:556856 CAPLUS <<LOGINID::20100206>>
DN 135:286235
TI Genomic and proteomic analysis of the myeloid differentiation program
AU Lian, Zheng; Wang, Le; Yamaga, Shigeru; Bonds, Wesley; Beazer-Barclay, Y.; Rüger, Yuval; Gerstein, Mark; Newburger, Peter E.; Berliner, Nancy; Weissman, Sherman M.
CS Department of Genetics, Boyer Center for Molecular Medicine, the Section of Hematology, Department of Internal Medicine, Yale University School of Medicine, New Haven, CT, 06536-0812, USA
SO Blood (2001), 98(3), 513-524 CODEN: BLOOAW; ISSN: 0006-4971
PB American Society of Hematology
DT Journal
LA English
AB Although the mature neutrophil is one of the better characterized mammalian cell types, the mechanisms of myeloid differentiation are incompletely understood at the mol. level. A mouse promyelocytic cell line (MPRO), derived from murine bone marrow cells and arrested developmentally by a dominant-neg. retinoic acid receptor, morphol. differentiates to mature neutrophils in the presence of 10.mu.M retinoic acid. An extensive catalog was prepd. of the gene expression changes that occur during morphol. maturation. To do this, 3'-end differential display, oligonucleotide chip array hybridization, and

2-dimensional protein electrophoresis were used. A large no. of genes whose mRNA levels are modulated during differentiation of MPRO cells were identified. The results suggest the involvement of several transcription regulatory factors not previously implicated in this process, but they also emphasize the importance of events other than the prodn. of new transcription factors. Furthermore, gene expression patterns were compared at the level of mRNA and protein, and the correlation between 2 parameters was studied.
CSC.G 66 THERE ARE 66 CAPLUS RECORDS THAT CITE THIS RECORD (66 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 182 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:554286 CAPLUS <<LOGINID::20100206>>
DN 136:15013
TI Autophagy Delays Sulindac Sulfide-Induced Apoptosis in the Human Intestinal Colon Cancer Cell Line HT-29
AU Bauvy, Chantal; Gane, Pierre; Arico, Sebastien; Codogno, Patrice; Ogier-Denis, Eric
CS INSERM U504 Glycobiologie et Signalisation Cellulaire, Villejuif, 94807, Fr.
SO Experimental Cell Research (2001), 268(2), 139-149
CODEN: ECREAL; ISSN: 0014-4827
PB Academic Press
DT Journal
LA English
AB Autophagy is a major catabolic process allowing the renewal of intracellular organelles by which cells maintain their homeostasis. We have previously shown that autophagy is controlled by two transduction pathways mediated by a heterotrimeric Gi3 protein and phosphatidylinositol 3-kinase activities in the human colon cancer cell line HT-29. Here, we show that 3-methyladenine, an inhibitor of autophagy, increases the sensitivity of HT-29 cells to apoptosis induced by sulindac sulfide, a nonsteroidal anti-inflammatory drug which inhibits the cyclooxygenases. Similarly, HT-29 cells over-expressing a GTPase-deficient mutant of the G.alpha.i3 protein (Q204L), which have a low rate of autophagy, were more sensitive to sulindac sulfide-induced apoptosis than parental HT-29 cells. In both cell populations we did not observe ***differences** in the ***expression** ***patterns** of COX-2, Bcl-2, BclXL, Bax, and Akt/PKB ***activity** . However, the rate of cytochrome c release was higher in Q204L-over-expressing cells than in HT-29 cells. These results suggest that autophagy could retard apoptosis in colon cancer cells by sequestering mitochondrial death-promoting factors such as cytochrome c. (c) 2001 Academic Press.
CSC.G 54 THERE ARE 54 CAPLUS RECORDS THAT CITE THIS RECORD (54 CITINGS)
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 183 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:544244 CAPLUS <<LOGINID::20100206>>
DN 135:255313
TI Overexpression of .alpha.4 chain-containing laminins in human glial tumors identified by gene microarray analysis
AU Ljubimova, Julia Y.; Lakhter, Alexander J.; Loksh, Anna; Yong, William H.; Riedinger, Mary S.; Miner, Jeffrey H.; Sorokin, Lydia M.; Ljubimov, Alexander V.; Black, Keith L.
CS Cedars-Sinai Medical Center, Maxine Dunitz Neurosurgical Institute, Los Angeles, CA, 90048, USA
SO Cancer Research (2001), 61(14), 5601-5610 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Differential gene expression in tumors often involves growth factors and extracellular matrix/basement membrane components. Here, 11,000-gene microarray was used to identify gene expression profiles in brain tumors including high-grade gliomas [glioblastoma multiforme (GBM) and anaplastic astrocytoma], low-grade astrocytomas, or benign extra-axial brain tumors (meningioma) in comparison with normal brain tissue. Histol. normal tissues adjacent to GBMs were also studied. All GBMs studied overexpressed 14 known genes compared with normal human brain tissue. Overexpressed genes belonged to two broad groups: (a) growth factor-related genes; and (b) structural/extracellular matrix-related genes. For most of these 14 genes, expression levels were lower in low-grade astrocytoma than in GBM and were barely detectable in normal brain. Despite normal-appearing histol., gene expression patterns of tissues immediately adjacent to GBM were similar to those of their resp. primary GBMs. Two genes were consistently up-regulated in both high-grade and low-grade gliomas, as well as in histol. normal tissues adjacent to GBMs. These genes coded for the epidermal growth factor receptor (previously reported to be overexpressed in gliomas) and for the .alpha.4 chain of laminin, a major blood vessel basement membrane component. Changes in expression of this laminin chain have not been previously assocd. with malignant tumors. Overexpression of laminin .alpha.4 chain in GBM and astrocytoma grade II by gene microarray anal. was confirmed by semiquantitative reverse transcription-PCR and immunohistochem. Importantly, an .alpha.4 chain-contg. laminin isoform, laminin-8 (.alpha.4.beta.1.gamma.1), was expressed mainly in blood vessel walls of GBMs and histol. normal tissues adjacent to GBMs, whereas another .alpha.4 chain-contg. laminin isoform, laminin-9 (.alpha.4.beta.2.gamma.1), was expressed mainly in blood vessel walls of low-grade tumors and normal brain. GBMs that overexpressed laminin-8 had a shorter mean time to tumor recurrence (4.3 mo) than GBMs with overexpression of laminin-9 (9.7 mo, P = 0.0007). Up-regulation of .alpha.4 chain-contg. laminins could be important for the development of glioma-induced neovascularization and glial tumor progression. Overexpression of laminin-8 may be predictive of glioma recurrence.
CSC.G 54 THERE ARE 54 CAPLUS RECORDS THAT CITE THIS RECORD (54 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 184 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:533410 CAPLUS <<LOGINID::20100206>>
DN 136:256687
TI Identification of cyclosporine A and tacrolimus glucuronidation in human liver and the gastrointestinal tract by a differentially expressed UDP-glucuronosyltransferase: UGT2B7
AU Strassburg, Christian P.; Barut, Ayse; Obermayer-Straub, Petra; Li, Qing; Nguyen, Nghia; Tukey, Robert H.; Manns, Michael P.
CS Department of Gastroenterology and Hepatology, Hannover Medical School, Hannover, 30625, Germany

SO Journal of Hepatology (2001), 34(6), 865-872 CODEN: JOHEEC; ISSN: 0168-8278
PB Elsevier Science Ltd.
DT Journal
LA English
AB The oral administration of the major transplant immunosuppressants cyclosporine A and tacrolimus leads to unpredictable drug levels requiring drug monitoring. Hepatic and extrahepatic metab. of cyclosporine A and tacrolimus by cytochrome P 450 proteins was analyzed but metab. and inactivation by glucuronidation was not investigated. Cyclosporine A and tacrolimus glucuronidation was measured in hepatic and gastrointestinal microsomal protein, and with 11 recombinant hepatic and extrahepatic family 1 and 2 UDP-glucuronosyltransferases. UDP-glucuronosyltransferase transcripts were detd. by polymerase chain reaction. Significant cyclosporine and tacrolimus glucuronidation activity was present in endoplasmic reticulum from liver, duodenum, jejunum, ileum, and colon, but was absent in stomach. Specific cyclosporine A glucuronidation activity was highest in liver and colon, tacrolimus glucuronidation was highest in liver. Analyses using recombinant UDP-glucuronosyltransferases identified UGT2B7 as a human UDP-glucuronosyltransferase with specific activity toward cyclosporine A and tacrolimus. The hepato-gastrointestinal distribution of immunosuppressant glucuronidation ***activity*** corresponded to the ***differential*** ***expression*** ***pattern*** of UGT2B7 mRNA. This study provides conclusive evidence of hepatic and extrahepatic immunosuppressant glucuronidation by human UGT2B7 which was identified to be differentially expressed in the human hepatogastrointestinal tract. Hepatic and extrahepatic glucuronidation may influence the therapeutic efficacy of transplant immunosuppressants.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 185 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:530788 CAPLUS <<LOGINID::20100206>>
DN 135:300002
TI Mechanism of cell cycle regulation by RB protein and E2F transcription factor
AU Ikeda, Masaaki
CS Graduate School of Medical and Dental Science, Tokyo Medical and Dental University, Japan
SO Wakaru Saibo Shuki to Gan (2000), 28-36. Editor(s): Taya, Yoichi. Publisher: Yodosha, Tokyo, Japan. CODEN: 69BNSV
DT Conference; General Review
LA Japanese
AB A review with refs., on RB protein and E2F transcription factor as regulatory mols. in S-phase progression; ***changes*** of RB family proteins in cell cycle; structures and ***expression*** ***pattern*** of E2F and DP family proteins; mechanism of E2F ***activity*** regulation; RB family protein suppression of E2F target genes; G1 cyclin/CDK activation of RB-E2F pathway; E2F in DNA replication; and RB-E2F pathway in neoplastic transformation and apoptosis.

L12 ANSWER 186 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:502885 CAPLUS <<LOGINID::20100206>>
DN 135:236639
TI Intracellular and extracellular control of activin function by novel regulatory molecules
AU Tsuchida, K.; Matsuzaki, T.; Yamakawa, N.; Liu, Z.; Sugino, H.
CS Institute for Enzyme Research, The University of Tokushima, Tokushima, 770-8503, Japan
SO Molecular and Cellular Endocrinology (2001), 180(1-2), 25-31 CODEN: MCENDG; ISSN: 0303-7207
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Activin signal transduction is regulated through multiple mechanisms. We have identified novel regulatory proteins that control activin functions either intracellularly or extracellularly. As intracellular mols., PSD-95/Dlg/ZO-1 (PDZ) proteins that specifically assoc. with activin type II receptors (ActRIIs) were identified. We have named the mols. as activin receptor-interacting proteins (ARIPs). ARIP1 has two WW domains and five PDZ domains, assocs. not only with ActRIIs but also with Smads, and controls activin functions intracellularly in neuronal cells. Another ARIP we have found has only one PDZ domain, and is likely to be involved in intracellular trafficking and sorting of activin receptor complexes in the cell. As an extracellular regulatory protein, we have identified a novel follistatin-like protein, named follistatin-related gene (FLRG). Like follistatins, FLRG binds activins and bone morphogenetic proteins (BMPs) and controls their functions extracellularly. The mode of assocn. of follistatin and FLRG with ***activins*** and their ***expression*** ***patterns*** are ***different*** , suggesting the distinct functions of follistatin and FLRG in vivo.
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 187 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:500949 CAPLUS <<LOGINID::20100206>>
DN 136:129604
TI DNA microarray analysis of genes involved in p53 mediated apoptosis: activation of Apaf-1
AU Kannan, Karuppiah; Kaminski, Naftali; Rechavi, Gideon; Jakob-Hirsch, Jasmine; Amariglio, Ninette; Givol, David
CS Department of Molecular Cell Biology, Weizmann Institute of Science, Rehovot, 76100, Israel
SO Oncogene (2001), 20(26), 3449-3455 CODEN: ONCNES; ISSN: 0950-9232
PB Nature Publishing Group
DT Journal
LA English
AB The transcription regulation activity of p53 controls cellular response to a variety of stress conditions, leading to growth arrest and apoptosis. Despite major progress in the understanding of the global effects of p53 on cellular function the pathways by which p53 activates apoptosis are not well defined. To study genes activated in the p53 induced apoptotic process, we used a mouse myeloid leukemic cell line (LTR6) expressing the temp.-sensitive p53 (val135) that undergoes apoptosis upon shifting the temp. to 32.degree.C. We analyzed the gene ***expression*** ***profile*** at ***different*** time points after p53 ***activation*** using oligonucleotide microarray capable of detecting .apprx. 11 000 mRNA species. Cluster anal. of the p53-regulated genes indicate a pattern of early and late induced sets of genes. We show that 91 and 44 genes were substantially up and down regulated, resp., by p53.

Functional classification of these genes reveals that they are involved in many aspects of cell function, in addn. to growth arrest and apoptosis. Comparison of p53 regulated gene expression profile in LTR6 cells to that of a human lung cancer cell line (H1299) that undergoes growth arrest but not apoptosis demonstrates that only 15% of the genes are common to both systems. This observation supports the presence of two distinct transcriptional programs in response to p53 signaling, one leading to growth arrest and the other to apoptosis. The proapoptotic genes induced only in LTR6 cells like Apaf-1, Sumo-1 and gelsolin among others may suggest a possible explanation for apoptosis in LTR6 cells.
OSC.G 93 THERE ARE 93 CAPLUS RECORDS THAT CITE THIS RECORD (94 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 188 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:468702 CAPLUS <<LOGINID::20100206>>
DN 136:18658
TI Differential gene expression profiling in human brain tumors
AU Markert, James M.; Fuller, Catherine M.; Gillespie, G. Yancey; Bubien, James K.; McLean, Lee Anne; Hong, Robert L.; Lee, Kailin; Gullans, Steven R.; Mapstone, Timothy B.; Benos, Dale J.
CS Department of Surgery, University of Alabama at Birmingham, Birmingham, AL, 35294-0005, USA
SO Physiological Genomics [online computer file] (2001), 5(1), 21-33 CODEN: PHGEFP; ISSN: 1094-8341 URL: http://physiolgenomics.physiology.org/cgi/reprint/5/1/21
PB American Physiological Society
DT Journal; (online computer file)
LA English
AB Gene expression profiling of three human temporal lobe brain tissue samples (normal) and four primary glioblastoma multiforme (GBM) tumors using oligonucleotide microarrays was done. Moreover, confirmation of altered expression was performed by whole cell patch clamp, immunohistochem. staining, and RT-PCR. Our results identified several ion and solute transport-related genes, such as N-methyl-D-aspartate (NMDA) receptors, .alpha.-amino-3-hydroxy-5-methyl-4-isoxazole propionate (AMPA)-2 receptors, GABAA receptor subunits .alpha.3, .beta.1, .beta.2, and .beta.3, the glutamate transporter, the glutamate/aspartate transporter II, the potassium channel Kv2.1, hKv9.3, and the sodium/proton exchanger 1 (NHE-1), that are all downregulated in the tumors compared with the normal tissues. In contrast, aquaporin-1, possibly aquaporins-3 and -5, and GLUT-3 message appeared upregulated in the tumors. Our results also confirmed previous work showing that osteopontin, nicotinamide N-methyltransferase, murine double minute 2 (MDM2), and epithelin (granulin) are upregulated in GBMs. We also demonstrate for the first time that the cytokine and p53 binding protein, macrophage migration inhibitory factor (MIF), appears upregulated in GBMs. These results indicate that the modulation of ion and solute transport genes and heretofore unsuspected cytokines (i.e., MIF) may have profound implications for brain tumor cell biol. and thus may identify potential useful therapeutic targets in GBMs.
OSC.G 107 THERE ARE 107 CAPLUS RECORDS THAT CITE THIS RECORD (107 CITINGS)
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 189 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:465882 CAPLUS <<LOGINID::20100206>>
DN 135:178761
TI A novel mechanism for chaperone-mediated telomerase regulation during prostate cancer progression
AU Akalin, Ali; Elmore, Lynne W.; Forsythe, Heidi L.; Amaker, Barbara A.; McCollum, Eric D.; Nelson, Peter S.; Ware, Joy L.; Holt, Shawn E.
CS Department of Pathology, Massey Cancer Center, Medical College of Virginia at Virginia Commonwealth University, Richmond, VA, 23298, USA
SO Cancer Research (2001), 61(12), 4791-4796 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Telomerase activity has been detected in >85% of all malignant human cancers, including 90% of prostate carcinomas. Using a well-characterized exptl. prostate cancer system, the authors have found that telomerase activity is notably increased (> 10-fold) during tumorigenic conversion. ***Expression*** ***profiles*** of the telomerase components (hTR and hTERT) revealed no substantive ***changes*** , which suggests a nontranscriptional mechanism for increased ***activity*** . Because the hsp90 chaperone complex functionally assocs. with telomerase, the authors investigated that relation and found that along with telomerase activity, a no. of hsp90-related chaperones are markedly elevated during transformation, as well as in advanced prostate carcinomas. Using the nontumorigenic cell protein ext. as the source of telomerase, addn. of purified chaperone components enhanced reconstitution of telomerase activity, which suggests a novel mechanism of increased telomerase assembly via a hsp90 chaperoning process during prostate cancer progression.
OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 190 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:456217 CAPLUS <<LOGINID::20100206>>
DN 135:177534
TI Identification of post-translationally modified proteins in proteome studies
AU Sickmann, Albert; Marcus, Katrin; Schafer, Heike; Butt-Dorje, Elke; Lehr, Stefan; Herkner, Armin; Suer, Silke; Bahr, Inke; Meyer, Helmut E.
CS Proteinstrukturlabor, Institut fur Physiologische Chemie, Ruhr-Universitat Bochum, Bochum, 44780, Germany
SO Electrophoresis (2001), 22(9), 1669-1676 CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
AB ***Proteome*** studies are powerful tools to solve many ***different*** problems in metab., signal transduction, ***drug*** discovery, and other areas of interest in life sciences. Up to now, high-sensitive methods for protein identification after two-dimensional gel electrophoresis using mass spectrometry are available. However, the identification of post-translational modifications after two-dimensional gel electrophoresis is still an unsolved problem. In this paper, we

want to give several examples for the successful identification of post-translational modifications and point mutations.
OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (28 CITINGS)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 191 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:438355 CAPLUS <<LOGINID::20100206>>
DN 136:117092
TI Global changes in interleukin-6-dependent gene expression patterns in mouse livers after partial hepatectomy
AU Li, Wei; Liang, Xianping; Leu, Julie I.; Kovalovich, Kellen; Qliberto, Gennaro; Taub, Rebecca
CS Department of Genetics, University of Pennsylvania Medical School, Philadelphia, PA, 19104, USA
SO Hepatology (Philadelphia, PA, United States) (2001), 33(6), 1377-1386 CODEN: HPTLD9; ISSN: 0270-9139
PB W. B. Saunders Co.
DT Journal
LA English
AB Liver regeneration following 70% partial hepatectomy leads to rapid activation of genes in the remnant liver. Interleukin-6 deficient (IL-6 -/-) mice have impaired liver regeneration and abnormalities in immediate early gene expression. Here, the gene expression program in the IL-6 +/+ and -/- livers at 2 h posthepatectomy was examd. with a cDNA array representing 588 highly regulated mouse genes. Thirty-six percent of the 103 immediate early genes were induced differently in IL-6 +/+ compared with IL-6 -/- livers, implying regulation by IL-6. IL-6 treatment of the IL-6 -/- mice in the absence of hepatectomy induced a much smaller set of genes in the liver, suggesting that IL-6 cooperates with other hepatectomy-induced factors to activate the large no. of genes. Northern blot analyses were used to verify gene expression data obtained from the arrays. The expression of urokinase type plasminogen activator receptor (uPAR) and plasminogen activator inhibitor-1 (PAI-1), crit. components of the urokinase plasminogen activator (uPA) system, was lower and delayed in IL-6 -/- livers. Despite the fact that active uPAR/uPA complex is crit. for hepatocyte growth factor (HGF) activation, no differences were detected between the IL-6 +/+ and -/- livers in HGF activation as measured by receptor phosphorylation. On the contrary, the mitogen-activated protein kinase (MAPK) pathway was activated in IL-6 +/+ livers early during regeneration but remarkably delayed in IL-6 -/- livers. Defective liver regeneration may be explained by the large no. of gene activation pathways altered in IL-6 -/- livers and further supports the finding that IL-6 is necessary for normal liver regeneration.
OSC.G 44 THERE ARE 44 CAPLUS RECORDS THAT CITE THIS RECORD (44 CITINGS)
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 192 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:374841 CAPLUS <<LOGINID::20100206>>
DN 135:119687
TI Stamina pistilloida, the pea ortholog of Fim and UFO, is required for normal development of flowers, inflorescences, and leaves
AU Taylor, Scott; Hofer, Julie; Murfet, Ian
CS School of Plant Science, University of Tasmania, Hobart, 7001, Australia
SO Plant Cell (2001), 13(1), 31-46 CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Physiologists
DT Journal
LA English
AB Isolation and characterization of two severe alleles at the Stamina pistilloida (Stp) locus reveals that Stp is involved in a wide range of developmental processes in the garden pea. The most severe allele, stp-4, results in flowers consisting almost entirely of sepals and carpels. Prodn. of ectopic secondary flowers in stp-4 plants suggests that Stp is involved in specifying floral meristem identity in pea. The stp mutations also reduce the complexity of the compd. pea leaf, and primary inflorescences often terminate prematurely in an aberrant sepaloid flower. In addn., stp mutants were shorter than their wild-type siblings due to a redn. in cell no. in their internodes. Fewer cells were also found in the epidermis of the leaf rachis of stp mutants. Examn. of the effects of stp-4 in double mutant combinations with af, tl, det, and veg2-2-mutations known to influence leaf, inflorescence, and flower development in pea-suggests that Stp function is independent of these genes. A synergistic interaction between weak mutant alleles at Stp and Uni indicated that these two genes act together, possibly to regulate primordial growth. Mol. anal. revealed that Stp is the pea homolog of the Antirrhinum gene Fimbriata (Fim) and of UNUSUAL FLORAL ORGANS (UFO) from Arabidopsis. ***Differences*** between Fim/UFO and Stp mutant phenotypes and ***expression*** ***patterns*** suggest that expansion of Stp ***activity*** into the leaf was an important step during evolution of the compd. leaf in the garden pea.
OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 193 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:293053 CAPLUS <<LOGINID::20100206>>
DN 135:3657
TI Proteomic profiling from human samples: the body fluid alternative
AU Kennedy, S.
CS The Forum, Oxford GlycoSciences (UK) Ltd, Abingdon, Oxon, OX14 4RY, UK
SO Toxicology Letters (2001), 120(1-3), 379-384 CODEN: TOLEDS; ISSN: 0378-4274
PB Elsevier Science Ireland Ltd.
DT Journal; General Review
LA English
AB A review with no refs. ***Proteomics*** is one of the technologies rapidly ***changing*** the authors' approach to ***drug*** development. The applications of proteomics, particularly with ref. to anal. of body fluid samples, will be described. Proteomic anal. involves the systematic sepn., identification and characterization of proteins present in a biol. sample. By comparing the proteins present in diseased samples with those present in normal samples, it is possible to identify changes in expression of proteins that potentially may be related to organ toxicity. Proteomics is regarded as a sister technol. to genomics. Although the pattern of gene activity will be abnormal in a tissue with a pathol. lesion, there can be a poor correlation between the level of activity of different genes and the relative

abundance within the tissue of the corresponding proteins. This is esp. true where the mode of action of the test material interferes with protein synthesis and/or post translational modification. Consequently, the information about a pathol. process that can be derived at the level of gene activity is incomplete. Proteomics has now made it possible to analyze proteins using high throughput, automated techniques. Although both mRNA and proteomic profiling can be applied to tissue samples, anal. of body fluids (e.g., serum, urine, CSF, synovial fluid) is restricted to proteomics. In these cases the protein compn. is derived from many tissues and processes. Proteomic anal. can yield information on disease processes and potential response to treatment. Examples will be presented of the identification of surrogate markers for hepatocellular carcinoma, breast cancer, from cerebrospinal fluid in humans and gentamicin toxicity in the rat.
OSC.G 80 THERE ARE 80 CAPLUS RECORDS THAT CITE THIS RECORD (80 CITINGS)

L12 ANSWER 194 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:164304 CAPLUS <<LOGINID::20100206>>
DN 134:250025
TI Differential Expression of Signal Transducers and Activators of Transcription during Human Adipogenesis
AU Harp, Joyce B.; Franklin, Dawn; Vanderpuije, Abenah A.; Gimble, Jeffrey M.
CS Department of Nutrition, University of North Carolina at Chapel Hill, NC, 27599, USA
SO Biochemical and Biophysical Research Communications (2001), 281(4), 907-912 CODEN: BBRCA9; ISSN: 0006-291X
PB Academic Press
DT Journal
LA English
AB Signal transducers and ***activators*** of transcription (STATs) display unique ***expression*** ***patterns*** upon induction of ***differentiation*** of murine 3T3-L1 preadipocytes into adipocytes. During differentiation, expression of STAT1 and STAT5 increase, while STAT3 and STAT6 remain relatively unchanged. Here, we detd. whether human s.c. preadipocytes expressed STATs and if the pattern of expression changed during adipogenesis. We found by Western blot anal. that freshly isolated preadipocytes expressed STAT1, STAT3, STAT5, and STAT6, but not STAT2 and STAT4. Induction of preadipocyte differentiation with 1-methyl-3-isobutylxanthine, dexamethasone, insulin, and BRL 49653 decreased expression of STAT1, and increased expression of STAT3 and STAT5. STAT6 expression did not change during adipogenesis. Changes in expression of CCAAT/enhancer binding protein .beta. (C/EBP.beta.), C/EBP.delta., C/EBP.alpha., and peroxisome proliferator-activated receptor .gamma. were similar to murine cell lines. These results suggest that unlike the traditional adipogenic transcription factors, unique differences exist in STAT expression patterns between murine and human adipose cells. (c) 2001 Academic Press.
OSC.G 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 195 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:65778 CAPLUS <<LOGINID::20100206>>
DN 135:32006
TI Gene expression profile changes in initiation and progression of squamous cell carcinoma of esophagus
AU Lu, Jiayun; Liu, Zhihua; Xiong, Momiao; Wang, Qun; Wang, Xiuqin; Yang, Guanrui; Zhao, Liqun; Qiu, Zongliang; Zhou, Chuannong; Wu, Min
CS National Laboratory of Molecular Oncology, Department of Cell Biology, Cancer Institute, Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, 100021, Peop. Rep. China
SO International Journal of Cancer (2001), 91(3), 288-294 CODEN: IJCNAW; ISSN: 0020-7136
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Tumorigenesis is a complex process involving multiple genes. As a step toward understanding the complicated changes between normal and malignant cells, this report focused on gene expression profile variations among normal and abnormal esophageal epithelium tissues. The cDNA microarray approach was used to investigate gene expression profiles of 5 different stages during initiation and progression of esophageal cancer. According to pathol. characteristics, these 5 stages were normal, dysplasia I (mild dysplasia), dysplasia II (moderate dysplasia), carcinoma in situ (CIS) and squamous cell carcinoma of esophagus (SCC). Comparing and analyzing those gene expression profiles, we obsd. that the expression levels of many genes changed in dysplasia I and some known tumor-related genes were over-expressed or under-expressed in all 4 abnormal stages. Using principal component anal. we identified a set of genes that may play an important role in tumor development. Hybridization data were confirmed by semi-quant. reverse transcription-polymerase chain reaction and immunohistochem. These results suggest that cDNA microarray technol. is a useful tool to discover genes frequently involved in esophageal neoplasia and provides novel clues to diagnosis, early detection and intervention of SCC.
OSC.G 55 THERE ARE 55 CAPLUS RECORDS THAT CITE THIS RECORD (55 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 196 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:60995 CAPLUS <<LOGINID::20100206>>
DN 135:119400
TI The transcriptional activator Cat8p provides a major contribution to the reprogramming of carbon metabolism during the diauxic shift in Saccharomyces cerevisiae
AU Haurie, Valerie; Perrot, Michel; Mini, Thierry; Jeno, Paul; Sagliocco, Francis; Boucherie, Helian
CS Institut de Biochimie et Genetique Cellulaires, UMR 5095, Bordeaux, 33077, Fr.
SO Journal of Biological Chemistry (2001), 276(1), 76-85 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB In yeast, the transition between the fermentative and the oxidative metab., called the diauxic shift, is assocd. with major changes in gene expression and protein synthesis. The zinc cluster protein Cat8p is required for the derepression of nine genes under nonfermentative growth conditions (ACS1, FBP1, ICL1, IDP2, JEN1, MLS1, PCK1, SFC1, and SIP4). To investigate whether the transcriptional control mediated by Cat8p can be extended to other genes and whether this control is the main

control for the changes in the synthesis of the resp. proteins during the adaptation to growth on ethanol, we analyzed the transcriptome and the proteome of a cat8.DELTA. strain during the diauxic shift. In this report, we demonstrate that, in addn. to the nine genes known as Cat8p-dependent, there are 25 other genes or open reading frames whose expression at the diauxic shift is altered in the absence of Cat8p. For all of the genes characterized here, the Cat8p-dependent control results in a parallel alteration in mRNA and protein synthesis. It appears that the biochem. functions of the proteins encoded by Cat8p-dependent genes are essentially related to the first steps of ethanol utilization, the glyoxylate cycle, and gluconeogenesis. Interestingly, no function involved in the tricarboxylic cycle and the oxidative phosphorylation seems to be controlled by Cat8p.
OSC.G 64 THERE ARE 64 CAPLUS RECORDS THAT CITE THIS RECORD (64 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 197 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:58144 CAPLUS <<LOGINID::20100206>>
DN 134:221254
TI Granulocyte-macrophage colony stimulating factor up-regulates CCR1 in human neutrophils
AU Cheng, Sara S.; Lai, Joyce J.; Lukacs, Nicholas W.; Kunkel, Steven L.
CS Department of Pathology and Graduate Program in Cellular and Molecular Biology, University of Michigan Medical Center, School of Public Health, University of Michigan, Ann Arbor, MI, 48109, USA
SO Journal of Immunology (2001), 166(2), 1178-1184 CODEN: JOIMAS; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB Neutrophils (polymorphonuclear leukocytes; PMN) are phagocytic cells instrumental in the clearance of infectious pathogens. Human PMN are commonly thought to respond primarily to chemokines from the CXC family. However, recent findings suggest that under specific cytokine activation conditions, PMN can also respond to some CC chemokines. Here, the effect of GM-CSF, a well-characterized PMN priming and maturation factor, on CC-chemokine receptor (CCR) expression in PMN was investigated. Constitutive expression of CCR1 and CCR3 mRNA in PMN was detected by RNase protection assay. Following incubation of PMN with GM-CSF (0.01-10 ng/mL; 6 h) CCR1 mRNA expression was rapidly (.apprx.1 h) up-regulated. In contrast, no induction of CCR2, CCR3, CCR4, or CCR5 mRNA was obsd. CCR1 protein was also up-regulated by GM-CSF stimulation. GM-CSF-induced up-regulation of CCR1 showed functional consequences because GM-CSF-treated PMN, but not control cells, responded to the CC chemokines macrophage inflammatory protein-1.alpha., monocyte chemoattractant protein-3, and RANTES in assays of chemotactic migration and intracellular calcium mobilization. Thus, PMN ***activated*** by the proinflammatory cytokine GM-CSF can ***change*** their receptor ***expression*** ***pattern*** and become responsive to CC chemokines.
OSC.G 51 THERE ARE 51 CAPLUS RECORDS THAT CITE THIS RECORD (51 CITINGS)
RE.CNT 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 198 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:41032 CAPLUS <<LOGINID::20100206>>
DN 135:3720
TI Variability in gene expression patterns of Ewing tumor cell lines differing in EWS-FLI1 fusion type
AU Aryee, Dave N. T.; Sommergruber, Wolfgang; Muehlbacher, Karin; Dockhorn-Dworniczak, Barbara; Zoubek, Andreas; Kovar, Heinrich
CS Children's Cancer Research Institute St. Anna Kinderspital, Vienna, A-1090, Austria
SO Laboratory Investigation (2000), 80(12), 1833-1844 CODEN: LAINAW; ISSN: 0023-6837
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB Type 1 and type 2 EWS-FLI1 fusion products result from variation in breakpoint locations arising from the t(11;22)(q24;q12) recurrent chromosomal translocation in Ewing's sarcoma family tumors (EFT). Previously, studies from our institution (updated in the present communication at a median follow-up of more than 6 yr) and others suggested a prognostic difference for EFT patients with localized disease depending on the type of EWS-FLI1 fusion present in the tumor. It has been suggested that the obsd. clin. discrepancies result from different transactivation potentials of the various EWS-FLI1 fusion proteins. In an attempt to identify genes whose expression levels are differentially modulated by structurally different EWS-FLI1 transcription factors, we have used two related PCR-based subtractive approaches, cDNA representational difference anal. (cDNA-RDA) and linker-capture subtraction (LCS) to compare transcript representations in cDNA pools of type 1 vs. type 2 EFT cell lines. About 800 clones obtained by the two approaches were analyzed by dot blot hybridization to cDNA pools. Eighty-six clones showing the highest variability in signal intensities on the dot blots were further hybridized to individual EFT cell line RNAs on Northern blots, and four of them were addnl. studied by real-time quant. PCR (RTQ-PCR). Although interindividual variations in gene expression patterns in the range of one- to several-fold were obsd., no correlation to specific EWS-FLI1 fusion types could be identified. Among the genes differentially expressed in individual EFT cell lines are several previously implicated in tumor growth, invasion, and metastasis. Although our data may have revealed candidate genes whose composite expression pattern may be relevant for the biol. of individual EFT, they do not support a role of distinct EWS-FLI1 fusion types for EFT prognosis based on different transactivation potentials.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 199 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:900813 CAPLUS <<LOGINID::20100206>>
DN 134:67182
TI Characterization of the yeast transcriptome and genes differentially expressed during the cell cycle
IN Velculescu, Victor; Vogelstein, Bert; Kinzler, Kenneth
PA Johns Hopkins University, USA
SO PCT Int. Appl., 419 pp. CODEN: PIXXD2
DT Patent

LA English PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------

PI WO 2000077214 A2 20001221 WO 2000-US16223 20000614 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG

PRAI US 1999-335032 19990616

AB The present invention discloses that certain hitherto unknown genes (termed NORFs, not previously assigned open reading frames) exist and are expressed in yeast. The present invention identifies which genes are differentially expressed during the cell cycle, and they are uniquely identified by their SAGE (serial anal. of gene expression) tags. Anal. of 60,633 transcripts revealed 4665 genes, with expression levels ranging from 0.3 to over 200 transcripts per cell. Of these genes, 1981 had known functions, while 2684 were previously uncharacterized. Integration of positional information with gene expression data allowed the generation of chromosomal expression maps, identifying phys. regions of transcriptional activity, and identified genes that had not been predicted by sequence information alone. These genes can be used to study, affect, and monitor the cell cycle of a eukaryotic cell. They can be used to obtain human homologs involved in cell cycle regulation. They can be used to identify antifungal agents and other classes of drugs. They can be formed into arrays on solid supports for interrogation of a cell's transcriptome under various conditions. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L12 ANSWER 200 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2000:882180 CAPLUS <<LOGINID::20100206>>

DN 134:172965

TI A functional genomic study of the effects of antipsychotic agent chlorpromazine in PC12 cells

AU Kontkanen, Outi; Lakso, Merja; Wong, Garry; Castren, Eero

CS Laboratory of Molecular Pharmacology, A.I.Virtanen Institute, University of Kuopio, Kuopio, Finland

SO Clinical Chemistry and Laboratory Medicine (2000), 38(9), 911-915 CODEN: CCLMFW; ISSN: 1434-6621

PB Walter de Gruyter GmbH & Co. KG

DT Journal

LA English

AB ***Expression*** ***profiling*** using methods of functional genomics can be used to investigate ***changes*** in gene transcription induced by ***drug*** treatment, which may lead to discovery of new potential drug targets. Antipsychotic agents alleviate symptoms of schizophrenia but the mechanism behind their clin. efficacy is unclear. We have used the PC12 cell line as a model to characterize effects of the antipsychotic drug chlorpromazine on gene expression using high-d. complementary DNA array filters prepd. from a rat brain entorhinal cortex complementary DNA library. Chlorpromazine treatment pos. regulated the expression of several clones, five of which were selected for further characterization. Northern blotting expts. confirmed the increased expression of these genes after chlorpromazine treatment. Sequencing revealed that two clones were cytochrome c oxidase and three were novel genes. Characterization of the function of these genes could increase our understanding of the mechanisms of action of antipsychotic drugs, and might be beneficial for the development of more effective agents.

OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 201 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2000:868962 CAPLUS <<LOGINID::20100206>>

DN 134:190579

TI Expression and immunodetection of a P-glycoprotein in emetine-resistant trophozoites of Entamoeba histolytica

AU Banuelos, Cecilia; Perez, D. Guillermo; Gomez, Consuelo; Orozco, Esther

CS Departamento de Patologia Experimental, Centro de Investigacion y de Estudios Avanzados del I.P.N. (Cinvestav), Mexico, Mex.

SO Archives of Medical Research (2000), 31(4, Suppl.), S288-S290 CODEN: AEDEER; ISSN: 0188-4409

PB Elsevier Science Inc.

DT Journal

LA English

AB A study was conducted to examine Entamoeba histolytica P-glycoprotein functions by generating antibodies against a recombinant P-glycoprotein polypeptide to first det. the expression level in sensitive and drug-resistant trophozoites. This is a step toward the detn. of the location and physiol. role of the P-glycoproteins in the multidrug resistance (MDR) phenotype in E. histolytica. Findings indicated that the ***differential*** P-glycoprotein ***expression*** ***patterns*** found by confocal microscopy correlate with the ***drug*** -resistant phenotype expressed in the three clones of E. histolytica.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 202 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2000:850761 CAPLUS <<LOGINID::20100206>>

DN 135:168

TI Analysis of drug pharmacology towards predicting drug behavior by expression profiling using high-density oligonucleotide arrays

AU Hu, Jing-Shan; Durst, Mark; Kerb, Reinhold; Truong, Vivi; Ma, Jing-Tyan; Khurgin, Elina; Balaban, David; Gingeras, Thomas R.; Hoffman, Brian B.

CS Affymetrix, Incorporated, Santa Clara, CA, 95051, USA

SO Annals of the New York Academy of Sciences (2000), 919(Toxicology for the Next Millennium), 9-15 CODEN: ANYAA9; ISSN: 0077-8923

PB New York Academy of Sciences

DT Journal

LA English

AB An important aspect of the drug development process is prediction of efficacious and toxic side effects. Profiling of mRNA expression is a powerful approach to analyze the mol. phenotype of cells under various conditions, for example, in response to stimulation by compds. We attempt to explore the approach of using expression profiling to identify patterns or fingerprints that are correlated with specific drug properties or behaviors.

Identification of such expression patterns may also lead to revelation of the potential action mechanism of drugs and fingerprints indicative of certain drug efficacy or side effects. We describe here a strategy that was used to identify a set of genes whose ***differential*** ***expression*** ***pattern*** correlates with ***activation*** mode and target specificity of a specific group of drug compds.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 203 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:840960 CAPLUS <<LOGINID::20100206>>
DN 134:113963
TI Differential pituitary gene expression profiles associated- to aging and spontaneous tumors as revealed by rat cDNA expression array
AU Goidin, Didier; Kappeler, Laurent; Perrot, Jacques; Epelbaum, Jacques; Gourdji, Danielle
CS U.159 INSERM IFR Broca-Sainte Anne, Paris, Fr.
SO Endocrinology (2000), 141(12), 4805-4808 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB Aging of the rat pituitary is often accompanied by the occurrence of adenomas. We asked whether complementary DNA hybridization array was adapted to identify gene expression patterns linked to aging and assocd. spontaneous adenomas. Thus, [32P]dATP-labeled cDNAs were prepd. from pituitaries of three month-old rats (Y) and tumor-bearing 20-28-mo-old rats (OT). The cDNAs were hybridized to identical membrane arrays allowing to study simultaneously 588 known genes (Clontech 7738-1). Among the 79 genes detected, the GH gene was predominantly expressed in both groups. Twenty-eight genes in the OT group and 15 in the Y group were found to be expressed at a higher level. The largest differences were of about 17 fold and were obsd. for the galanin and glutathione S transferase genes in the Y and OT groups, resp. Relative RT-PCR was applied to validate the OT vs. Y expression pattern obtained via cDNA array hybridization. The results were consistent for 14 out the 15 genes tested. In the light of these results, differential membrane array hybridization appears suitable to identify gene expression profiles assocd. with pituitary aging.
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 204 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:834408 CAPLUS <<LOGINID::20100206>>
DN 135:86273
TI Differential gene expression technologies for identifying surrogate markers of drug efficacy and toxicity
AU Rininger, J. A.; DiPippo, V. A.; Gould-Rothberg, B. E.
CS CuraGen Corporation, New Haven, CT, 06511, USA
SO Drug Discovery Today (2000), 5(12), 560-568 CODEN: DDTOFS; ISSN: 1359-6446
PB Elsevier Science Ltd.
DT Journal; General Review
LA English
AB A review with 46 refs. Advances in the rapidly evolving discipline of pharmacogenomics have forced the biotechnol. and pharmaceutical industries to integrate ***differential*** gene ***expression*** ***profiling*** into their ***drug*** discovery and development strategies. Here we highlight the use of differential gene expression technologies for the elucidation of both drug efficacy and toxicity as well as novel candidate genes for pharmacogenetic analyses to assess individual variability to drug response. This will include an overview of the different technologies created to facilitate pharmacogenomic analyses and to highlight advantages and disadvantages of these emerging methodologies. Two high-throughput differential gene expression technologies, microarrays and GeneCalling.RTM., will be presented in detail.
OSC.G 35 THERE ARE 35 CAPLUS RECORDS THAT CITE THIS RECORD (35 CITINGS)
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 205 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:763064 CAPLUS <<LOGINID::20100206>>
DN 134:3028
TI Analysis of three Ptx2 splice variants on transcriptional ***activity*** and ***differential*** ***expression*** ***pattern*** in the brain
AU Smidt, Marten P.; Cox, Joke J.; Van Schaick, Hermien S. A.; Coolen, Marcel; Schepers, Janneke; Van der Kleij, Arno M.; Burbach, J. Peter H.
CS Section of Molecular Neuroscience, Department of Medical Pharmacology, Rudolf-Magnus Institute for Neurosciences, Utrecht University Medical Center, Utrecht, 3584 CG, Neth.
SO Journal of Neurochemistry (2000), 75(5), 1818-1825 CODEN: JONRA9; ISSN: 0022-3042
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB Three different transcripts of the homeodomain gene termed pituitary homeobox (Ptx) 2 (Ptx2/Brx/Rieg/Solurshin/Arp) were cloned from different species encoding proteins belonging to the paired-like family of homeodomain proteins. Ptx2a (324 amino acids), Ptx2b (271 amino acids), and Ptx2c (318 amino acids) share the C terminus, including the homeodomain, and have different N termini. Here we report the comparative anal. of all three ***different*** Ptx2 splice variants for their transcriptional ***activity*** and their ***expression*** ***pattern*** in the adult rat brain. Ptx2 is able to trans-activate via different model promoters in different cell lines. A mild difference in trans-activating potential is obsd. among the splice variants, but the underlying mechanism is at present unknown. It is surprising that all Ptx2 transcripts displayed an identical expression pattern in the brain. This markedly restricted pattern is limited to the following brain areas: the anterior and intermediate lobes of the pituitary gland, the subthalamic nucleus, the posterior hypothalamic nucleus, the mammillary bodies, the red nucleus, and the deep gray layer of the superior colliculus. The data presented suggest that all variants of Ptx2 are involved in the development and regulation of distinct neuronal cell groups and the pituitary gland.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 206 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:716965 CAPLUS <<LOGINID::20100206>>
DN 135:41531
TI A transient assay for regulatory gene function in haemopoietic progenitor cells
AU McIvor, Zoe J.; Heyworth, Clare M.; Johnson, Barbra A.; Pearson, Stella; Fiegler, Heike; Hampson, Lynn; Dexter, T. Michael; Cross, Michael A.
CS Laboratory of Molecular Medicine, IZKF University of Leipzig, Leipzig, 04103, Germany
SO British Journal of Haematology (2000), 110(3), 674-681
CODEN: BJHEAL; ISSN: 0007-1048
PB Blackwell Science Ltd.
DT Journal
LA English
AB This work aimed to provide a means of assaying directly the effects of transient expression of introduced genes on the survival, proliferation, lineage commitment and differentiation of hemopoietic progenitor cells. For this purpose, the authors developed a system that allows isolation of productively transfected, multipotent hemopoietic cells within a few hours of the introduction of test genes. FDCP-mix cells productively transfected with expression plasmids encoding green fluorescent protein (GFP) differentiate normally and retain colony-forming potential. The authors constructed an expression vector consisting of a bicistronic cassette in which a GFP marker gene and a test gene are driven from the same promoter. The vector design has been optimized for co-expression and the test gene was shown to be biol. active. The ***expression*** ***profile*** from a transiently transfected template under ***different*** growth conditions reveals that ***active*** expression continues for at least 2 d after transfection. The transient transfection of FDCP-mix cells with the vectors described provides a powerful tool for anal. of the immediate early effects of test gene overexpression during hemopoietic differentiation.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 207 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:671516 CAPLUS <<LOGINID::20100206>>
DN 134:127912
TI Proteomics: New tools for a new era
AU Edwards, Aled M.; Arrowsmith, Cheryl H.; Des Pallieres, Bertrand
CS Ontario Cancer Institute and the Banting and Best Department of Medical Research, University of Toronto, Toronto, ON, Can.
SO Modern Drug Discovery (2000), 3(7), 35,38,41-42,44
CODEN: MDDIFT; ISSN: 1099-8209
PB American Chemical Society
DT Journal; General Review
LA English
AB A review with 14 refs. The primary goal of proteomics is to provide functional annotations for the entire proteome. The function of a protein has many definitions, ranging from its biochem. ***activity*** to its physiol. role, and so the optimal ***proteomics*** strategy must integrate many ***different*** technologies. This article is an overview of the technologies most relevant to the drug discovery process, and it gives some ideas about developing proteomics technologies.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 208 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:603875 CAPLUS <<LOGINID::20100206>>
DN 134:53568
TI Expression of the hepatitis E virus ORF1
AU Ropp, S. L.; Tam, A. W.; Beames, B.; Purdy, M.; Frey, T. K.
CS Department of Biology, Georgia State University, Atlanta, GA, USA
SO Archives of Virology (2000), 145(7), 1321-1337 CODEN: ARVDF; ISSN: 0304-8608
PB Springer-Verlag Wien
DT Journal
LA English
AB Hepatitis E virus (HEV) is an unclassified, plus-strand RNA virus whose genome contains three open reading frames (ORFs). ORF1, the 5' proximal ORF of HEV, encodes nonstructural proteins involved in RNA replication which share homol. with the products of the corresponding ORF of members of the alphavirus-like superfamily of plus-strand RNA viruses. Among animal virus members of this superfamily (the alphavirus and rubivirus genera of the family Togaviridae), the product of this ORF is a nonstructural polyprotein (NSP) that is cleaved by a papain-like cysteine protease (PCP) within the NSP. To det. if the NSP of HEV is similarly processed, ORF1 was introduced into a plasmid vector which allowed for expression both in vitro using a coupled transcription/translation system and in vivo using a vaccinia virus-driven transient expression system. A recombinant vaccinia virus expressing ORF1 was also constructed. Both in vitro and in vivo expression under std. conditions yielded only the full-length 185 kDa polyprotein. Addn. of co-factors in vitro, such as divalent cations and microsomes which have been shown to ***activate*** other viral proteases, failed to ***change*** this ***expression*** ***pattern*** . However, in vivo following extended incubations (24-36 h), two potential processing products of 107 kDa and 78 kDa were obsd. N- and C-terminus-specific immunopptn. and deletion mutagenesis were used to det. that the order of these products within the NSP is NH2-78 kDa-107 kDa-COOH. However, site-specific mutagenesis of Cys483, predicted by computer alignment to be one member of the catalytic dyad of a PCP within the NSP, failed to abolish this cleavage. Addnl. sequence alignment across HEV strains revealed that the other member of the proposed catalytic dyad of this PCP, His590, was not conserved. Thus, the cleavage of the NSP obsd. following prolonged in vivo expression was not mediated by this protease and it is doubtful that a functional PCP exists within the NSP. Attempts to detect NSP expression and processing in HEV-infected primary monkey hepatocytes were not successful and therefore this proteolytic cleavage could not be authenticated. Overall, the results of this study indicate that either the HEV NSP is not processed or that it is cleaved at one site by a virally-encoded protease novel among alpha-like superfamily viruses or a cellular protease.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 209 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2000:536987 CAPLUS <<LOGINID::20100206>>
DN 134:16107
TI Expression profile of transcripts in Alzheimer's disease tangle-bearing CA1 neurons
AU Ginsberg, Stephen D.; Hemby, Scott E.; Lee, Virginia M.-Y.; Eberwine, James H.; Trojanowski, John Q.
CS Center for Neurodegenerative Disease Research, Department of Pathology and Laboratory Medicine, University of Pennsylvania School of Medicine, Philadelphia, PA, USA
SO Annals of Neurology (2000), 48(1), 77-87 CODEN: ANNED3; ISSN: 0364-5134
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB The pathogenesis of neurofibrillary tangles (NFTs) in Alzheimer's disease (AD) is poorly understood, but changes in the expression of specific mRNAs (mRNAs) may reflect mechanisms underlying the formation of NFTs and their consequences in affected neurons. For these reasons, we compared the relative abundance of multiple mRNAs in tangle-bearing vs. normal CA1 neurons aspirated from sections of AD and control brains. Amplified antisense RNA expression profiling was performed on individual isolated neurons for anal. of greater than 18,000 expressed sequence tagged cDNAs with cDNA microarrays, and further quant. analyses were performed by reverse Northern blot anal. on 120 selected mRNAs on custom cDNA arrays. Relative to normal CA1 neurons, those harboring NFTs in AD brains showed significant redns. in several classes of mRNAs that are known to encode proteins implicated in AD neuropathol., including phosphatases/kinases, cytoskeletal proteins, synaptic proteins, glutamate receptors, and dopamine receptors. Because cathepsin D mRNA was upregulated in NFT-bearing CA1 neurons in AD brains, we performed immunohistochem. studies that demonstrated abundant cathepsin D immunoreactivity in the same population of tangle-bearing CA1 neurons. In addn., levels of mRNAs encoding proteins not previously implicated in AD were reduced in CA1 tangle-bearing neurons, suggesting that these proteins (e.g., activity-regulated cytoskeleton-assocd. protein, focal adhesion kinase, glutaredoxin, utrophin) may be novel mediators of NFT formation or degeneration in affected neurons. Thus, the profile of mRNAs differentially expressed by tangle-bearing CA1 neurons may represent a "mol. fingerprint" of these neurons, and we speculate that mRNA expression profiles of diseased neurons in AD may suggest new directions for AD research or identify novel targets for developing more effective AD therapies.
OSC.G 174 THERE ARE 174 CAPLUS RECORDS THAT CITE THIS RECORD (174 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 210 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:435160 CAPLUS <<LOGINID::20100206>>
DN 133:346062
TI A new member of acid-sensing ion channels from pituitary gland
AU Grunder, Stefan; Geissler, Hyun-Soon; Bassler, Eva-Lotta; Ruppersberg, J. Peter
CS Department of Otolaryngology, Section of Sensory Biophysics, Tubingen, D-72076, Germany
SO NeuroReport (2000), 11(8), 1607-1611 CODEN: NERPEZ; ISSN: 0959-4965
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB Acid-sensing ion channels (ASICs) constitute a branch of the super-gene family of amiloride-sensitive sodium channels. So far five different ASICs have been cloned from mammalian tissues. They are ***activated*** by a drop of extracellular pH but ***differ*** with respect to effective agonist concn., desensitization and mRNA ***expression*** ***pattern*** . Here we report cloning of ASIC4, a new protein showing about 45% identity to other ASICs. ASIC4 is 97% identical between rat and human and shows strongest expression in pituitary gland. Moreover, we detected expression throughout the brain, in spinal cord, and inner ear. ASIC4 cannot be activated by a drop of extracellular pH in Xenopus oocytes, suggesting assocn. with other subunits or activation by a ligand different from protons. Our results suggest a role for ASICs also in endocrine glands.
OSC.G 76 THERE ARE 76 CAPLUS RECORDS THAT CITE THIS RECORD (77 CITINGS)
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 211 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:394863 CAPLUS <<LOGINID::20100206>>
DN 133:279776
TI Two-dimensional gel electrophoresis analysis of the proteomes expressed in the human hepatoma cell line BEL-7404 and normal liver cell line L-02
AU Yu, Lirong; Wang, Nan; Wu, Gaode; Xu, Yonghua; Xia, Qichang
CS Shanghai Institute of Biochemistry, Chinese Academy of Sciences, Shanghai, 200031, Peop. Rep. China
SO Chinese Science Bulletin (2000), 45(12), 1113-1122 CODEN: CSBUEF; ISSN: 1001-6538
PB Science in China Press
DT Journal
LA English
AB Proteome anal. technol. has been used extensively in conducting discovery research of biol. and has become one of the most essential technologies in functional genomics. The proteomes of the human hepatoma cell line BEL-7404 and the normal human liver cell line L-02 were sepd. by high resoln. two-dimensional gel electrophoresis (2-DE) with immobilized pH gradient isoelec. focusing (IPG-IEF) in the first dimension and SDS-PAGE in the second dimension (IPG-DALT). The resulting images were analyzed using 2-D anal. software. Quant. anal. reveals that 7 protein spots were detected only in hepatoma BEL-7404 cells and 14 only in L-02 cells; 78 protein spots show significant fluctuation in quantity in both cell lines. These protein spots were displayed on a proteome differential expression map. Anal. for the reproducibility of 2-DE indicates that the positional variability in the IEF dimension is 0.73 mm, whereas the variability in the SDS-PAGE dimension is 0.44 mm, and the quant. variability is 17.6%-19.2%. Apparently, the reproducibility of 2-DE has been suitable for the study of differential expression of proteomes. ***Proteome*** ***differential*** expression maps can be useful tools for disease diagnosis, ***drug*** -target validation anal. and biol. process elucidation.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 212 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 2000:365550 CAPLUS <<LOGINID::20100206>>
DN 133:118595
TI Genomic views of the immune system
AU Staudt, Louis M.; Brown, Patrick O.
CS Metabolism Branch, Division of Clinical Sciences, National Cancer Institute, National Institutes of Health, Bethesda, MD, USA
SO Annual Review of Immunology (2000), 18, 829-859 CODEN: ARIMDU; ISSN: 0732-0582
PB Annual Reviews Inc.
DT Journal; General Review
LA English
AB A review with 109 refs. Genomic-scale experimentation aims to view biol. processes as a whole, yet with mol. precision. Using massively parallel DNA microarray technol., the mRNA expression of tens of thousands of genes can be measured simultaneously. Math. distn. of this flood of gene expression data reveals a deep mol. and biol. logic underlying gene expression programs during cellular differentiation and activation. Genes that encode components of the same multi-subunit protein complex are often coordinately regulated. Coordinate regulation is also obsd. among genes whose products function in a common differentiation program or in the same physiol. response pathway. Recent application of gene ***expression*** ***profiling*** to the immune system has shown that lymphocyte ***differentiation*** and ***activation*** are accompanied by changes of hundreds of genes in parallel. The databases of gene expression emerging from these studies of normal immune responses will be used to interpret the pathol. changes in gene expression that accompany autoimmunity, immune deficiencies, and cancers of immune cells.
OSC.G 106 THERE ARE 106 CAPLUS RECORDS THAT CITE THIS RECORD (106 CITINGS)
RE.CNT 110 THERE ARE 110 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 213 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:358265 CAPLUS <<LOGINID::20100206>>
DN 133:100802
TI mRNA expression patterns in different stages of asbestos-induced carcinogenesis in rats
AU Sandhu, H.; Dehnen, W.; Roller, M.; Abel, J.; Unfried, K.
CS Department of Experimental Toxicology, Medical Institute of Environmental Hygiene at the Heinrich Heine University, Duesseldorf, 40225, Germany
SO Carcinogenesis (2000), 21(5), 1023-1029 CODEN: CRNGDP; ISSN: 0143-3334
PB Oxford University Press
DT Journal
LA English
AB Human malignant mesotheliomas are induced almost exclusively by fibrous dusts. The nature of interactions between fibers and target cells, and the mol. mechanisms leading to tumorigenesis, are not yet understood. Here, the mRNA expression patterns at different stages of asbestos-induced carcinogenesis in rats were monitored by suppression subtractive hybridization (SSH) and array assay. Several genes were upregulated in pre-tumorous tissues from asbestos-treated rats, in asbestos-induced tumors, and in cells treated with asbestos in vitro. The upregulation of the proto-oncogene c-myc, fra-1, and egfr in fiber-induced carcinogenesis was demonstrated at different stages of carcinogenesis. A possible role of Fra-1 as one of the dimeric proteins generating the AP-1 transcription factor was substantiated by its dose-dependent expression in mesothelial cells treated with asbestos in vitro. The upregulation of osteopontin (an extracellular matrix protein) and of zyxin and integrin-linked kinase (intracellular proteins assocd. with the focal adhesion contact) indicate that fibers may affect integrin-linked signal transduction and extracellular matrix proteins.
OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 214 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:325757 CAPLUS <<LOGINID::20100206>>
DN 133:72635
TI Regulation of alternative splicing of CD45 by antagonistic effects of SR protein splicing factors
AU ten Dam, Gerdy B.; Zilch, Christian F.; Wallace, Diana; Wieringa, Be; Beverley, Peter C. L.; Poels, Lambert G.; Screaton, Gavin R.
CS Department of Cell Biology, University of Nijmegen, Nijmegen, 6500 HB, Neth.
SO Journal of Immunology (2000), 164(10), 5287-5295 CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB CD45 is a transmembrane glycoprotein possessing tyrosine phosphatase activity, which is involved in cell signaling. CD45 is expressed on the surface of most leukocytes and can be alternatively spliced by the indusion or skipping of three variable exons (4, 5, and 6 or A, B, and C) to produce up to eight isoforms. In T cells, the splicing pattern of CD45 isoforms changes after activation; naive cells express high m.w. isoforms of CD45 which predominantly express exon A (CD45RA), whereas activated cells lose expression of exon A to form low m.w. isoforms of CD45 including CD45RO. Little is known about the specific factors controlling the switch in CD45 splicing which occurs on activation. In this study, the authors examd. the influence of the SR family of splicing factors, which, like CD45, are expressed in tissue-specific patterns and have been shown to modulate the alternative splicing of a variety of transcripts. The authors show that specific SR proteins have antagonistic effects on CD45 splicing, leading either to exon inclusion or skipping. Furthermore, the authors were able to demonstrate specific ***changes*** in the SR protein ***expression*** ***pattern*** during T cell ***activation***
OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (28 CITINGS)
RE.CNT 67 THERE ARE 67 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 215 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:322960 CAPLUS <<LOGINID::20100206>>
DN 133:277074
TI Structure of the mouse NDRF gene and its regulation during neuronal differentiation of P19 cells
AU Oda, H.; Iwata, I.; Yasunami, M.; Ohkubo, H.
CS Institute of Molecular Embryology and Genetics, Kumamoto University School of Medicine, Kumamoto, Japan
SO Molecular Brain Research (2000), 77(1), 37-46 CODEN: MBREE4; ISSN: 0169-328X
PB Elsevier Science B.V.
DT Journal

LA English
AB We have isolated and characterized the mouse gene for NDRF (neuroD-related factor), a basic helix-loop-helix transcription factor implicated in neural development and function. The gene consists of two exons and the entire protein-coding sequence is encoded by a single downstream exon. RNA blot hybridization anal. revealed that NDRF mRNA was detectable at day 4 and increased to a maximal level at day 6 during neuronal differentiation of P19 cells. To elucidate the regulatory mechanisms of the NDRF gene expression during this process, a construct contg. the genomic DNA fragment of about 3 kbp upstream of the NDRF coding region fused to a luciferase reporter gene was transfected into P19 cells, and stable transformants were pooled for assay of luciferase activities. When the stable transformants were treated with RA and aggregated to induce neuronal ***differentiation*** , the luciferase ***activities*** were induced in a temporal ***expression*** ***pattern*** similar to that of the endogenous NDRF mRNA. Further expts. using a series of deletion and mutation constructs indicated that the 376-bp sequence in the 5'-flanking region of the NDRF gene is important, and that one of the E boxes in the sequence plays a crit. role in the regulated expression. Transient transfection expts. also showed that the same E box is required for the transactivation of the NDRF promoter activity by neurogenin 1. These results suggest that the NDRF gene expression is regulated by an E box-binding factor during neuronal differentiation of P19 cells.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 216 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:287336 CAPLUS <<LOGINID::20100206>>
DN 133:71701
TI The birth of muscle progenitor cells in the mouse. Spatiotemporal considerations
AU Tajbakhsh, Shahragim; Buckingham, Margaret
CS Department of Molecular Biology, Pasteur Institute, Paris, 75724, Fr.
SO Current Topics in Developmental Biology (2000), 48(Somitogenesis, Pt. 2), 225-268 CODEN: CTDBA5; ISSN: 0070-2153
PB Academic Press
DT Journal; General Review
LA English
AB A review with refs. is given concerning primarily with the spatiotemporal dynamics of gene expression patterns in the somite, in muscle progenitor cells, and their derivs., skeletal muscles. The following issues are considered: origins of skeletal muscle in vertebrates; domains of the dermomyotome; ***differences*** between somites at ***different*** axial levels; myogenic regulatory factor ***expression*** ***patterns*** in the somite and myotome heterogeneity; somite ***differentiation*** and ***activation*** of Myf5 and MyoD by extrinsic factors; the roles of Myf5 and MyoD in defining different subpopulations of muscle cells and in muscle progenitor cell detn. (c) 2000 Academic Press.
OSC.G 93 THERE ARE 93 CAPLUS RECORDS THAT CITE THIS RECORD (93 CITINGS)
RE.CNT 165 THERE ARE 165 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 217 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:212858 CAPLUS <<LOGINID::20100206>>
DN 132:342612
TI Integrating expression-based drug response and SNP-based pharmacogenetic strategies into a single comprehensive pharmacogenomics program
AU Rothberg, Bonnie E. Gould; Ramesh, Tennore M.; Burgess, Catherine E.
CS CuraGen Corp., New Haven, CT, 06511, USA
SO Drug Development Research (2000), 49(1), 54-64 CODEN: DDREDK; ISSN: 0272-4391
PB Wiley-Liss, Inc.
DT Journal; General Review
LA English
AB A review with many refs. In the third millennium, competitive advantage in drug development will derive from expertise in two areas: 1) the ability to prioritize and triage hits from a combinatorial chem./high-throughput screening expt. and pursue only those hits most likely to succeed through clin. development, and 2) the ability to identify those patients capable of mounting a therapeutic response with minimal toxic effects. Pharmacogenomics, the branch of genomics addressing mol. pharmacol. and toxicol., is anticipated to streamline drug development by addressing these issues. Pharmacogenomics includes two sep. disciplines: expression pharmacogenomics and pharmacogenetics. Typically, they are regarded as unique fields and are pursued independently from each other. Here, we describe a pharmacogenomic strategy that combines and integrates both fields to create a single robust program. GeneCalling, a rapid, comprehensive ***differential*** transcript ***expression*** ***profiling*** technique, is applied to rodent models of ***drug*** response to identify novel markers predictive of drug efficacy and toxicity. SeqCalling, a high-throughput transcript sequencing strategy with a coding region bias, has identified 120,000 novel human single nucleotide polymorphisms (SNPs). Novel pharmacogenetic candidates are then identified by searching the human ortho-logs of rodent drug response genes for SeqCalling SNPs that can be pursued in systematic genotype screens to verify clin. correlations. In this manner, GeneCalling expression pharmacogenomics identifies markers capable of triaging leads from hits and SeqCalling converts a subset of these markers into pharmacogenetic correlates capable of identifying appropriately responsive patients.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 218 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:198886 CAPLUS <<LOGINID::20100206>>
DN 132:329270
TI Harnessing the power of the genome in the search for new antibiotics
AU Rosamond, John; Allsop, Aileen
CS AstraZeneca, Macclesfield, Cheshire, SK10 4TG, UK
SO Science (Washington, D. C.) (2000), 287(5460), 1973-1976 CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal; General Review
LA English
AB A review with 35 refs. Over the past 40 yr, the search for new antibiotics has been largely restricted to well-known compd.

classes active against a std. set of drug targets. Although many effective compds. have been discovered, insufficient chem. variability has been generated to prevent a serious escalation in clin. resistance. Recent advances in genomics have provided an opportunity to expand the range of potential drug targets and have facilitated a fundamental shift from direct antimicrobial screening programs toward rational target-based strategies. The application of genome-based technologies such as ***expression*** ***profiling*** and ***proteomics*** will lead to further ***changes*** in the ***drug*** discovery paradigm by combining the strengths and advantages of both screening strategies in a single program.
OSC.G 113 THERE ARE 113 CAPLUS RECORDS THAT CITE THIS RECORD (113 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 219 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:189713 CAPLUS <<LOGINID::20100206>>
DN 133:87055
TI Identification of a mouse germ cell-less homolog with conserved activity in Drosophila
AU Leatherman, J. L.; Kaestner, K. H.; Jongens, T. A.
CS Department of Genetics, University of Pennsylvania School of Medicine, Philadelphia, PA, USA
SO Mechanisms of Development (2000), 92(2), 145-153
CODEN: MEDVE6; ISSN: 0925-4773
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Drosophila Germ cell-less (Gcl) has previously been shown to be important in early events during the formation of pole cells, which are the germ cell precursors in the fly. We have isolated a 524 amino acid mouse gene with 32% identity and 49% similarity to Drosophila gcl, termed mgcl-1. Like Drosophila Gcl, mGcl-1 localizes to the nuclear envelope. Ectopic expression of mgcl-1 in Drosophila rescues the gcl-null phenotype, indicating that mGcl-1 is a functional homolog of Gcl. MGcl-1 maps to chromosome 6 at 47.3 cM, and is expressed at low levels at all embryonic stages examd. from 8.5 to 18.5 d.p.c. as well as in many adult tissues. Different from Drosophila gcl, mgcl-1 is not highly expressed at the time the primordial germ cells appear in the mouse, but high mgcl-1 expression is found in selected mouse adult male germ cells. The ***differences*** in these ***expression*** ***patterns*** in light of conserved ***activity*** between the two genes is discussed.
OSC.G 23 THERE ARE 23 CAPLUS RECORDS THAT CITE THIS RECORD (23 CITINGS)
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 220 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:173674 CAPLUS <<LOGINID::20100206>>
DN 133:75
TI Expression profiling in toxicology - potentials and limitations
AU Steiner, S.; Anderson, N. L.
CS Large Scale Biology Corporation, Rockville, MD, USA
SO Toxicology Letters (2000), 112-113, 467-471 CODEN: TOLED5; ISSN: 0378-4274
PB Elsevier Science Ireland Ltd.
DT Journal; General Review
LA English
AB A review and discussion with 16 refs. Recent progress in genomics and proteomics technologies has created a unique opportunity to significantly impact the pharmaceutical drug development processes. The perception that cells and whole organisms express specific inducible responses to stimuli such as drug treatment implies that unique expression patterns, mol. fingerprints, indicative of a drug's efficacy and potential toxicity are accessible. The integration into state-of-the-art toxicol. of assays allowing one to profile treatment-related ***changes*** in gene ***expression*** ***patterns*** promises new insights into mechanisms of ***drug*** action and toxicity. The benefits will be improved lead selection, and optimized monitoring of drug efficacy and safety in pre-clin. and clin. studies based on biol. relevant tissue and surrogate markers.
OSC.G 45 THERE ARE 45 CAPLUS RECORDS THAT CITE THIS RECORD (45 CITINGS)
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 221 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:145943 CAPLUS <<LOGINID::20100206>>
DN 133:53475
TI Pharmacogenomics of the cystic fibrosis transmembrane conductance regulator (CFTR) and the cystic fibrosis drug CPX using genome microarray analysis
AU Srivastava, Meera; Eidelman, Ofer; Pollard, Harvey B.
CS Department of Anatomy and Cell Biology, and Institute for Molecular Medicine, USU School of Medicine, USUHS, Bethesda, MD, 20814, USA
SO Molecular Medicine (New York) (1999), 5(11), 753-767
CODEN: MOMEF3; ISSN: 1076-1551
PB Springer-Verlag New York Inc.
DT Journal
LA English
AB Background: Cystic fibrosis (CF) is the most common lethal recessive disease affecting children in the U.S. and Europe. For this reason, a no. of ongoing attempts are being made to treat the disease either by gene therapy or pharmacotherapy. Several phase 1 gene therapy trials have been completed, and a phase 2 clin. trial with the xanthine drug CPX is in progress. The protein coded by the principal CFTR mutation, .DELTA.F508-CFTR, fails to traffic efficiently from the endoplasmic reticulum to the plasma membrane, and is the pathogenic basis for the missing cAMP-activated plasma membrane chloride channel. CPX acts by binding to the mutant .DELTA.F508-CFTR and correcting the trafficking deficit. CPX also activates mutant CFTR channels. The comparative genomics of wild-type and mutant CFTR has not previously been studied. However, we have hypothesized that the gene ***expression*** ***patterns*** of human cells expressing mutant or wild-type CFTR might ***differ*** , and that a ***drug*** such as CPX might convert the mutant gene expression pattern into one more characteristic of wild-type CFTR. To the extent that this is true, a pharmacogenomic profile for such corrective drugs might be deduced that could simplify the process of drug discovery for CF. Materials and Methods: To test this hypothesis we used cDNA microarrays to study global gene expression in human cells permanently transfected with either wild-type or mutant CFTR. We also tested the effects of CPX on global gene expression when incubated with cells expressing either mutant or wild-type CFTR. Results: Wild-type and mutant .DELTA.F508-CFTR induce distinct and differential changes in cDNA microarrays, significantly affecting up to 5% of the total genes in the array. CPX also induces substantial mutation-dependent and -independent changes in gene

expression. Some of these changes involve movement of gene expression in mutant cells in a direction resembling expression in wild-type cells. Conclusions: These data clearly demonstrate that cDNA array anal. of cystic fibrosis cells can yield useful pharmacogenomic information with significant relevance to both gene and pharmacol. therapy. We suggest that this approach may provide a paradigm for genome-based surrogate endpoint testing of CF therapeutics prior to human administration.
OSC.G 40 THERE ARE 40 CAPLUS RECORDS THAT CITE THIS RECORD (41 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 222 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:131760 CAPLUS <<LOGINID::20100206>>
DN 133:13286
TI Molecular characterization of ubiquitin genes from Aspergillus nidulans: mRNA expression on different stress and growth conditions
AU Noventa-Jordao, M. A.; do Nascimento, A. M.; Goldman, M. H. S.; Terenzi, H. F.; Goldman, G. H.
CS Faculdade de Ciencias Farmaceuticas de Ribeirao Preto, Departamento de Ciencias Farmaceuticas, Universidade de Sao Paulo, Universidade de Franca, Sao Paulo, CEP 14040-903, Brazil
SO Biochimica et Biophysica Acta, Gene Structure and Expression (2000), 1490(3), 237-244 CODEN: BBGSD5; ISSN: 0167-4781
PB Elsevier B.V.
DT Journal
LA English
AB We are interested in studying the ubiquitin (UBI) gene expression during different stress and growth conditions in the filamentous fungus Aspergillus nidulans. Here, we report the cloning of a cDNA clone that corresponds to a gene, ubi1, that encodes a carboxyl extension protein from A. nidulans. This cDNA corresponds to a gene that encodes a protein that showed high homol. to other polyubiquitin and CEP-80 genes at the N- and C-terminus, resp. We characterize the mRNA expression of the CEP and polyubiquitin genes during several growth and stress conditions. Expression of the ubi1 and ubi4 genes was correlated with cell growth in most of the carbon sources used, except maltose. Both ubi1 and ubi4 genes were induced upon heat-shock, although the levels of expression were raised quicker for ubi4 than for ubi1. The ubi1 and ubi4 genes displayed a very complex ***expression*** ***pattern*** in presence of ***drugs*** with a ***different*** mechanism of action suggesting that the regulatory processes controlling UBI gene expression discriminate between different stresses and can affect individually each UBI gene. The ubi1 gene was highly expressed in presence of hydrogen peroxide while the ubi4 mRNA level was not affected; several metals in our exptl. conditions were not able to induce either ubi1 nor ubi4 genes.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 223 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:116274 CAPLUS <<LOGINID::20100206>>
DN 133:41304
TI Different expression profiles of human cyclin B1 in normal PHA-stimulated T lymphocytes and leukemic T cells
AU Viallard, Jean-Francois; Lacombe, Francis; Dupouy, Maryse; Ferry, Helene; Belloc, Francis; Reiffers, Josy
CS Laboratoire de Greffe de Moelle, UMR-CNRS 5540, Bordeaux, Fr.
SO Cytometry (2000), 39(2), 117-125 CODEN: CYTODQ; ISSN: 0196-4763
PB Wiley-Liss, Inc.
DT Journal
LA English
AB In a previous work, flow cytometry (FCM) methods demonstrated that accumulation of human cyclin B1 in leukemic cell lines begins during the G1 phase of the cell cycle. In the present study, FCM was used to compare the localization and the kinetic patterns of cyclin B1 expression in Jurkat leukemia cell line and phytohemagglutinin (PHA)-stimulated normal T lymphocytes. Cell synchronization was performed in G1 with sodium n-butyrate, at the G1/S transition with thymidine and at mitosis with colchicine. Cells (leukemic cell line Jurkat or PHA-stimulated human T-lymphocytes) were stained for DNA and cyclin B1 and analyzed by FCM. Western blotting was used to confirm certain results. Under asynchronous growing conditions and for both cell populations, cyclin B1 expression was essentially restricted to the G2/M transition, reaching its maximal level at mitosis. When the cells were synchronized at the G1/S boundary by thymidine or inside the G1 phase by sodium n-butyrate, Jurkat cells accumulated cyclin B1 in both situations, whereas T lymphocytes expressed cyclin B1 only during the thymidine block. The cyclin B1 fluorescence kinetics of PHA-stimulated T lymphocytes was strictly similar when considering T lymphocytes blocked at the G1/S phase transition by thymidine and in exponentially growing conditions. These FCM results were confirmed by Western blotting. The detection of cyclin B1 by Western blot in cells sorted in the G1 phase of the cell cycle showed that cyclin B1 was present in the G1 phase in leukemic T cells but not in normal T lymphocytes. Cyclin B1 degrdn. was effective at mitosis, thus ruling out a defective cyclin B1 proteolysis. The leukemic T cells behaved quite differently from the untransformed T lymphocytes. Apparently, human cyclin B1 is present in the G1 phase of the cell cycle in leukemic T cells but not in normal T lymphocytes. Therefore, the restriction point from which cyclin B1 can be detected is different in the two models studied. The authors hypothesize that after passage through a restriction point differing in T lymphocytes and in leukemic cells, the rate of cyclin B1 synthesis becomes const. in the S and G2/M phases and independent from the DNA replication cycle.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 224 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:74153 CAPLUS <<LOGINID::20100206>>
DN 132:263026
TI Differential Expression of the Transcription Factor NF-.kappa.B during Human Mononuclear Phagocyte Differentiation to Macrophages and Dendritic Cells
AU Ammon, Christoph; Mondal, Krishna; Andreesen, Reinhard; Krause, Stefan W.
CS Department of Hematology and Oncology, University of Regensburg, Regensburg, D-93042, Germany
SO Biochemical and Biophysical Research Communications (2000), 268(1), 99-105 CODEN: BBRCA9; ISSN: 0006-291X
PB Academic Press
DT Journal

LA English
AB An important role for the Rel/NF-.kappa.B family of transcription factors in the differentiation process of dendritic cells (DC) and macrophages (MAC) was recently suggested by a no. of mouse knockout studies, but only little information is available for defined populations of human cells. To investigate the role of individual NF-.kappa.B proteins [p50, p52, p65 (RelA), RelB] in the ***differentiation*** of monocyte-derived cell types we analyzed and compared the ***expression*** ***pattern*** and DNA binding ***activity*** of NF-.kappa.B members in human monocytes (MO), MO-derived MAC, and MO-derived DC. Constitutive expression of p65 and RelB mRNA was found in MO, and no significant regulation was obsd. during differentiation of MO into MAC or immature DC. Only during lipopolysaccharide-induced terminal differentiation of DC was a marked increase in RelB mRNA detected. In DNA binding assays performed with nuclear exts. from blood MO, p50/p50 homodimers were mainly detected, whereas complexes contg. p50/RelB and p50/p65 heterodimers were less abundant. DNA-bound protein complexes contg. p50/RelB and p50/p65 increased and addnl. p65/p65 complexes appeared during differentiation of MO into either MAC or immature DC. A strong increase in complexes contg. p50/RelB was obsd. during terminal differentiation of DC. Therefore, gradual differences in the DNA binding activities of different NF-.kappa.B homo- and heterodimers correlate with differentiation stages of MO, MAC, and DC and are probably important for the biol. role of these cells. (c) 2000 Academic Press.
CSC.G 57 THERE ARE 57 CAPLUS RECORDS THAT CITE THIS RECORD (57 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 225 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:793509 CAPLUS <<LOGINID::20100206>>
DN 132:133936
TI A novel glycosyltransferase with a polyglutamine repeat; a new candidate for GD1.alpha. synthase (ST6GalNAc V)
AU Ikehara, Y.; Shimizu, N.; Kono, M.; Nishihara, S.; Nakanishi, H.; Kitamura, T.; Narimatsu, H.; Tsuji, S.; Tatematsu, M.
CS Chikusa-ku, Division of Pathology, Aichi Cancer Center Research Institute, Nagoya, Japan
SO FEBS Letters (1999), 463(1,2), 92-96 CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB The fifth type GalNAc.alpha.2,6-sialyltransferase (mST6GalNAc V) was cloned from a mouse brain cDNA library. MST6GalNAc V exhibited type II transmembrane topol. contg. a polyglutamine repeat, which showed 42.6% and 44.8% identity to mouse ST6GalNAc III and IV, resp. Northern blot anal. revealed that the mST6GalNAc V gene was specifically expressed in forebrain and cerebellum. MST6GalNAc V exhibited GD1.alpha. synthetic activity from GM1b the same as mST6GalNAc III and IV. The ***activity*** ratio of GM1b toward fetuin and the ***expression*** ***pattern*** were completely ***different*** among the three ST6GalNAcs. Interestingly, the polyglutamine repeat no. was different from that of inbred mice. We report the first glycosyltransferase with a polymorphic polyglutamine repeat.
CSC.G 25 THERE ARE 25 CAPLUS RECORDS THAT CITE THIS RECORD (25 CITINGS)
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 226 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:688598 CAPLUS <<LOGINID::20100206>>
DN 132:120308
TI Protein kinase C activity regulates slow myosin heavy chain 2 gene expression in slow lineage skeletal muscle fibers
AU Dimario, Joseph X.; Funk, Phillip E.
CS Department of Cell Biology and Anatomy, The Chicago Medical School, North Chicago, IL, 60064, USA
SO Developmental Dynamics (1999), 216(2), 177-189 CODEN: DEDYEI; ISSN: 1058-8388
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Expression of the slow myosin heavy chain (MyHC) 2 gene defines slow vs. fast avian skeletal muscle fiber types. Fetal, or secondary, skeletal muscle fibers express slow MyHC isoform genes in developmentally regulated patterns within the embryo, and this patterning is at least partly dependent on innervation in vivo. We have previously shown that slow MyHC 2 gene expression in vitro is regulated by a combination of innervation and cell lineage. This pattern of gene expression was indistinguishable from the pattern obsd. in vivo in that it was restricted to innervated muscle fibers of slow muscle origin. We show here that slow MyHC 2 gene expression in the slow muscle fiber lineage is regulated by protein kinase C (PKC) activity. Inhibition of PKC activity induced slow MyHC 2 gene expression, and the capacity to express the slow MyHC 2 gene was restricted to muscle fibers of slow muscle (medial adductor) origin. Fast muscle fibers derived from the pectoralis major did not express significant levels of slow MyHC 2 with or without inhibitors of PKC activity. This ***differential*** ***expression*** ***pattern*** coincided with ***different*** inherent PKC ***activities*** in fast vs. slow muscle fiber types. Furthermore, overexpression of an unregulated PKC.alpha. mutant suppressed slow MyHC 2 gene expression in muscle fibers of the slow lineage. Lastly, denervation of skeletal muscles caused an increase in PKC activity, particularly in the slow medial adductor muscle. This increase in PKC activity was assocd. with lack of slow MyHC 2 gene expression in vivo. These results provide a mechanistic link between innervation, an intracellular signaling pathway mediated by PKC, and expression of a muscle fiber type-specific contractile protein gene.
CSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 227 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:657687 CAPLUS <<LOGINID::20100206>>
DN 133:15475
TI Immunohistochemical characterization of DU-PAN-2 expression in endometrial adenocarcinomas associated with CA19-9 expression
AU Muramatsu, Toshinari; Yasuda, Masanori; Itoh, Jobbu; Kamoshida, Shingo; Hirasawa, Takeshi; Murakami, Masaru; Shinozuka, Takao; Osamura, R. Yoshiyuki; Makino, Tsunehisa
CS Departments of Gynecology and Obstetrics, School of Medicine Tokai University, Kanagawa, 259-1193, Japan

SO Applied Immunohistochemistry & Molecular Morphology (1999), 7(3), 173-180 CODEN: AIMMFN
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB We analyzed the expression of DU-PAN-2 (Sialyl-Lewisc) and CA19-9 (Sialyl-Lewisa) immunohistochem. in a total of 133 operated cases of endometrial adenocarcinoma (EMA). These cases were histol. divided into three groups: grade 1 (G1), ltoreq.5% of a nonsquamous or nonmorular solid growth pattern (71 cases); grade 2 (G2), 6-50% of a nonsquamous or nonmorular solid growth pattern (34 cases); and grade 3 (G3), >50% of a nonsquamous or nonmorular growth pattern (28 cases). The immunoreactivity ratios of DU-PAN-2 and CA19-9 were G1: 81.7% (58/71) for DU-PAN-2, 70.4% (50/71) for CA19-9; G2: 76.5% (26/34) for DU-PAN-2, 47.1% (16/34) for CA19-9; G3: 60.7% (17/28) for DU-PAN-2, 32.1% (9/28) for CA19-9. DU-PAN-2 was expressed in 76.0% (19/25) of premenopausal cases and in 83.3% (65/78) of postmenopausal cases, and CA19-9 was expressed in 60.0% (15/25) of premenopausal cases and in 61.5% (48/78) of postmenopausal cases, indicating no significant differences in expression of these antigens between both groups. The difference between immunoreactivity ratios of DU-PAN-2 and CA19-9 tended to increase as EMAs became less differentiated, resulting in the predominance of DU-PAN-2 expression in G3. EMAs pos. for DU-PAN-2 exhibited a more favorable clin. outcome than those neg. for this antigen. The similar tendency was noted in the survival curves with CA19-9. We concluded that DU-PAN-2 expression was more frequent than that of CA19-9 in EMAs of various grades, with no correlation to menopausal status, and would be more specific for less differentiated EMAs. These antigen ***expression*** ***patterns*** might be assocd. with ***changes*** in Lewis enzyme ***activity***

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 228 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:623777 CAPLUS <<LOGINID::20100206>>
DN 132:234477
TI CEPU-1, an immunoglobulin superfamily molecule, has cell adhesion activity and shows dynamic expression patterns in chick embryonic spinal cord
AU Kimura, Y.; Shirabe, K.; Fukushima, M.; Takeshita, M.; Tanaka, H.
CS Division of Developmental Neurobiology, Kumamoto University Graduate School of Medical Sciences, Kumamoto, Japan
SO Neuroscience Research (Shannon, Ireland) (1999), 34(4), 245-255 CODEN: NERADN; ISSN: 0168-0102
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB To isolate novel mols. involved in motoneuron differentiation and target muscle innervation during embryogenesis, the authors performed mRNA differential display anal. by comparing cDNAs of motoneurons purified by immunopanning from different portions along the rostro-caudal axis of chick embryonic spinal cord, and cloned an Ig superfamily protein named C301. By sequence comparison, C30 was shown to be an alternatively spliced isoform of CEPU-1, which was formerly reported as a member of the Ig superfamily specifically expressed in cerebellar Purkinje cells (Spaltmann and Brummendorf, 1996, J. Neurosci. 16, 1770-1779). The authors analyzed the expression pattern of CEPU-1 both at the mRNA and protein levels in the spinal cord of the chick embryo. Until stage 23, CEPU-1 was expressed faintly in the ventral part of the neural tube but gradually it became localized to a specific group of cells. In the motor column, CEPU-1 was expressed transiently in many columnar layers. A C30-transfected cell line showed Ca2+-independent cell-cell binding activity. These results suggest a role for CEPU-1 in specific axon guidance and/or fasciculation of motoneurons during development.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 229 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:606333 CAPLUS <<LOGINID::20100206>>
DN 131:296788
TI Competitive binding of calmodulin isoforms to calmodulin-binding proteins: implication for the function of calmodulin isoforms in plants
AU Lee, Sang Hyoung; Kim, Min Chul; Heo, Won Do; Kim, Jong Cheol; Chung, Woo Sik; Park, Chan Young; Park, Hyeong Cheol; Cheong, Yong Hwa; Kim, Cha Young; Lee, Sung-Ho; Lee, Kyung Joo; Bahk, Jeong Dong; Lee, Sang Yeol; Cho, Moo Je
CS Department of Biochemistry, Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju, 660-701, S. Korea
SO Biochimica et Biophysica Acta, Protein Structure and Molecular Enzymology (1999), 1433(1-2), 56-67 CODEN: BBAEDZ; ISSN: 0167-4838
PB Elsevier B.V.
DT Journal
LA English
AB In plants, multiple calmodulin (CaM) isoforms exist in an organism which vary in their primary structures in as much as 32 residues out of their 148 amino acids. These CaM isoforms show ***differences*** in their ***expression*** ***patterns*** and/or target enzyme ***activation*** ability. To further understand the biol. significance of CaM isoforms, the authors examd. whether CaM isoforms act on specific regulatory targets. In gel overlay assays on various soybean tissue exts., surprisingly, two soybean CaM isoforms (SCaM-1 and SCaM-4) did not show significant differences in their target binding protein profiles, although they exhibited minor differences in their relative target binding affinities. In addn., both SCaM isoforms not only effectively bound five known plant CaMBPs, but also showed competitive binding to these proteins. Finally, immunolocalization expts. with the SCaM proteins in sections of various tissues using specific antibodies revealed similar distribution patterns for the SCaM isoforms except for root tissues, which indicates that the SCaM isoforms are concomitantly expressed in most plant tissues. These results suggest that CaM isoforms may compete for binding to CaMBPs in vivo. This competitive nature of CaM isoforms may allow modulation of Ca2+/CaM signaling pathways by virtue of relative abundance and differential target activation potency.
OSC.G 32 THERE ARE 32 CAPLUS RECORDS THAT CITE THIS RECORD (32 CITINGS)
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 230 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:597970 CAPLUS <<LOGINID::20100206>>
DN 131:227490
TI Characterization of a novel human surface molecule selectively expressed by mature thymocytes, activated T cells, and subsets of T cell lymphomas
AU Buonfiglio, Donatella; Bragardo, Manuela; Bonissoni, Sara; Redoglia, Valter; Cauda, Roberto; Zupo, Simona; Burgio, Vito L.; Wolff, Henrik; Fransslla, Kaarle; Gaidano, Gianluca; Carbone, Antonio; Janeway, Charles A., Jr.; Dianzani, Umberto
CS Dep. Medical Sciences, "A. Avogadro" Univ., Novara, I-28100, Italy
SO European Journal of Immunology (1999), 29(9), 2863-2874
CODEN: EJIMAF; ISSN: 0014-2980
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
AB The authors have previously characterized mouse H4 (mH4), a surface glycoprotein recognized by the C398.4A monoclonal antibody. The authors now show that C398.4A also binds its human putative homolog (hpH4). Both hpH4 and mH4 (1) are selectively expressed by activated T cells and mature thymocytes, (2) are disulfide-linked dimers of 2 chains (29/37 kDa in humans, 25/29 kDa in mice), whose N-deglycosylation produces a single band at 20-21 kDa, and (3) display a low associn. with CD4 and the TCR. The ***expression*** ***pattern*** of hpH4 and its biochem. features showed that it is ***different*** from other known ***activation*** mols., and this was confirmed when anal. of the tryptic digest of the hpH4 29-kDa band by peptide mass searching using matrix-assisted laser desorption ionization mass spectrometry did not reveal any significant homol. with other mols. In normal lymphoid tissue, hpH4 is expressed by T cells located at the periphery of lymph node germinal centers and paracortical areas. In T cell neoplasia, expression of hpH4 clusters with a subset of peripheral T cell lymphomas with a large-cell component, and with cases of angioimmunoblastic T cell lymphomas. These data provide evidence for a novel T cell activation mol. that could help in the phenotypic categorization of T cell malignancies.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 231 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:586151 CAPLUS <<LOGINID::20100206>>
DN 132:87851
TI Comparison of differential gene expression profiles in human esophageal squamous carcinoma EC8712 cells before and after arsenic trioxide (As2O3) treatment
AU Xie, Dongxu; Ding, Fang; Wang, Xiuqin; Liu, Zhihua; Luo, Aiping; Wu, Min
CS National Laboratory of Molecular Oncology, Department of Cell Biology, Cancer Institute, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, 100021, Peop. Rep. China
SO Chinese Science Bulletin (1999), 44(17), 1581-1587 CODEN: CSBUEF; ISSN: 1001-6538
PB Science in China Press
DT Journal
LA English
AB To elucidate mol. mechanisms of As2O3-induced apoptosis of cancer cells in vitro, Atlas human cDNA expression anal. was used for the profile of the known genes expressed in the human esophageal squamous carcinoma cells before and after treated by As2O3. On treating EC8712 cells with As2O3, most of the oncogenes were down-regulated, while some tumor suppressor genes, such as DCC, were up-regulated. Cyclin H decreased, whereas guanine nucleotide-releasing protein CDC25 increased. Heat-shock protein 86, a stress response protein, increased, suggesting that As2O3 has a toxic effect on cells. Most stimulating cell reprodn. factors were down-regulated. Many apoptosis-related proteins were up-regulated. DNA repair protein hMLH1 and DNase X were up-regulated. Most transcription factors and general DNA binding proteins regulated upward. ICH-2 protease (ICErel-II) and apopain, cysteine protease Mch2 isoform .beta. rose. Results indicated that As2O3 may induce change of expression of many genes and many genes may be involved in the process of apoptosis induced by As2O3. These findings provide further evidence that As2O3 might be clin. useful in solid tumor treatment.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 232 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:506917 CAPLUS <<LOGINID::20100206>>
DN 132:73307
TI Expression of Bcl-2 family proteins during chemotherapeutic agents-induced apoptosis in the hepatoblastoma Hep G2 cell line
AU Luo, Dan; Cheng, Samuel C. S.; Xie, Yong
CS Department of Biology, The Hong Kong University of Science and Technology, Hong Kong, Peop. Rep. China
SO British Journal of Biomedical Science (1999), 56(2), 114-122
CODEN: BJMSEO; ISSN: 0967-4845
PB Royal Society of Medicine Press Ltd.
DT Journal
LA English
AB This study demonstrates that 2 anticancer drugs, taxol and doxorubicin (Dox), can kill human hepatoblastoma Hep G2 cells in a dose-dependent manner via the induction of apoptosis. Characteristic events, including externalization of phosphatidylserine, cytoplasmic shrinkage, chromatin condensation, and DNA degrdn., were obsd. in a large majority of the drug-treated cells. DNA fragmentation showed that a ladder of DNA fragments of .apprx.200 bp multiples was obsd. in taxol-treated, but not in Dox-treated, cells. In addn., the expression patterns of Bcl-2 family members during taxol or Dox treatment were investigated. Results from Western blot anal. indicated that Hep G2 cells did not express either the death repressor Bcl-2, or the death promoters Bcl-XS and Bax. However, during the apoptotic process, one death repressor, Bcl-XL, and 2 death promoters, Bak and Bad, were expressed. The expression levels of Bcl-XL and Bak remained unchanged whereas the level of Bad was down-regulated. As the ratio between death repressors and death promoters in the Bcl-2 family will det. the sensitivity of cells to apoptotic stimuli, the findings suggest that the ***changed*** ***expression*** ***patterns** of Bcl-2 family proteins caused by anticancer ***drugs** in liver cancer cells may be involved in chemoresistance.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 233 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN

AN 1999:390223 CAPLUS <<LOGINID::20100206>>
DN 131:197067
TI Expression of Vp1 and water channel proteins during seed germination
AU Fukuhara, T.; Kirch, H.-H.; Bohnert, H. J.
CS Department of Biochemistry, The University of Arizona, Tucson, AZ, 85721-0088, USA
SO Plant, Cell and Environment (1999), 22(4), 417-424 CODEN: PLCEDV; ISSN: 0140-7791
PB Blackwell Science Ltd.
DT Journal
LA English
AB Germination of seeds from individual seed capsules of Mesembryanthemum crystallinum (common ice plant) is spread out over time with some seeds germinating within 1 d (early, E) and others germinating up to more than 4 wk after imbibition (late, L). L-seeds are characterized by a lack of expression of Cdc2-related transcripts and an increase of Vp1-transcripts after water uptake, while Cdc2-related transcripts increase early and Vp1 decline early in E-seeds. Maintenance of Vp1 transcription, which can be disrupted by abolishing translation activity, seems to be at the basis of prolonged dormancy in L-seeds. We have in addn. characterized the expression of several MIP (water channel) proteins during germination and in organs of adult plants. Using probes specific for individual ice plant Mip, we obsd. differences during germination that are not exclusively due to water uptake. Mip transcripts increase before L-seeds begin to germinate. Gene-specific probes indicate that the expression of all Mip is high in germinating seedlings, but differences in expression exist in the root, hypocotyl and cotyledon. In adult plants, all Mip-transcripts are expressed at a significantly lower rate than in seedlings, and organ-specific expression of individual Mip transcripts is obsd. Their ***expression***, ***measured*** by MIP-specific antibodies, indicates developmental specificity of MIP in ***different*** organs and highest amts. in ***actively*** growing tissues.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 234 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:318717 CAPLUS <<LOGINID::20100206>>
DN 131:165056
TI A comparative study of the effects of genistein and 2-methoxyestradiol on the proteolytic balance and tumor cell proliferation
AU Fajardo, I.; Quesada, A. R.; De Castro, I. Nunez; Sanchez-Jimenez, F.; Medina, M. A.
CS Laboratorio de Bioquimica y Biologia Molecular, Facultad de Ciencias, Universidad de Malaga, Malaga, E-29071, Spain
SO British Journal of Cancer (1999), 80(1/2), 17-24 CODEN: BJCAAI; ISSN: 0007-0920
PB Churchill Livingstone
DT Journal
LA English
AB The cytotoxicity of 2 compds. described as anti-angiogenic, the isoflavone genistein and the estrogen metabolite 2-methoxyestradiol, was studied in different human tumor cell lines. Since the degrdn. of the extracellular matrix is one of the essential steps in angiogenesis, the potential modulatory effects of both compds. on the proteolytic balance in media conditioned by different human tumor cells have been also investigated. The IC50 values for 2-methoxyestradiol were lower than those for genistein on all the cell lines tested. In all the cell lines ***expressing*** ***measurable*** amts. of ***active*** enzymes, genistein induced a ***shift*** towards antiproteolysis in both matrix metalloproteinase/tissue inhibitor of metalloproteinase and urokinase/plasminogen activator inhibitor proteolytic balances. On the other hand, 2-methoxyestradiol did not produce any clear net shift of the proteolytic balance, with the significant exception of the matrix metalloproteinase/tissue inhibitor of metalloproteinase balance in WAC-2 cells, a neuroblastoma cell line with enhanced expression of the N-myc oncogene.
OSC.G 25 THERE ARE 25 CAPLUS RECORDS THAT CITE THIS RECORD (25 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 235 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:272545 CAPLUS <<LOGINID::20100206>>
DN 131:54482
TI Influence of low temperature on productivity, proteome and protein phosphorylation of CHO cells
AU Kaufmann, Hitto; Mazur, Xenia; Fussenegger, Martin; Bailey, James E.
CS Institute of Biotechnology, ETH, Zurich, CH-8093, Switz.
SO Biotechnology and Bioengineering (1999), 63(5), 573-582 CODEN: BIBIAU; ISSN: 0006-3592
PB John Wiley & Sons, Inc.
DT Journal
LA English
AB Proliferation of mammalian cells can be controlled by low cultivation temp. However, depending on cell type and expression system, varying effects of a temp. shift on heterologous protein prodn. have been reported. Here, the authors characterize growth behavior and productivity of the Chinese hamster ovary (CHO) cell line XM111-10 engineered to synthesize the model-product-secreted alk. phosphatase (SEAP). Shift of cultivation temp. from 370C to 30.degree.C caused a growth arrest mainly in the G1 phase of the cell cycle concomitant with an up to 1.7-fold increase of specific productivity. A low temp. cultivation provided 3.4 times higher overall product yield compared to a std. cultivation at 37.degree.C. The cellular and mol. mechanisms underlying the effects of low temp. on growth and productivity of mammalian cells are poorly understood. Sepn. of total protein exts. by two-dimensional gel electrophoresis showed altered expression levels of CHO-K1 proteins after decrease in cultivation temp. to 300C. These ***changes*** in the ***proteome*** suggest that mammalian cells respond ***actively*** to low temp. by synthesizing specific cold-inducible proteins. In addn., the authors provide the first evidence that the cold response of mammalian cells includes changes in post-translational protein modifications. Two CHO proteins were found to be phosphorylated at tyrosine residues following downshift of cultivation temp. to 30.degree.C. Elucidating cellular events during cold exposure is necessary for further optimization of host-cell lines and expression systems and can provide new strategies for metabolic engineering.
OSC.G 99 THERE ARE 99 CAPLUS RECORDS THAT CITE THIS RECORD (99 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 236 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:214748 CAPLUS <<LOGINID::20100206>>
DN 130:350169
TI Cellular distribution and developmental expression of AMP-activated protein kinase isoforms in mouse central nervous system
AU Turnley, Ann M.; Stapleton, David; Mann, Richard J.; Witters, Lee A.; Kemp, Bruce E.; Bartlett, Perry F.
CS The Walter and Eliza Hall Institute of Medical Research, Royal Melbourne Hospital, Fitzroy, 3050, Australia
SO Journal of Neurochemistry (1999), 72(4), 1707-1716
CODEN: JONRA9; ISSN: 0022-3042
PB Lippincott Williams & Wilkins
DT Journal
LA English
AB The mammalian AMP-activated protein kinase is a heterotrimeric serine/threonine protein kinase with multiple isoforms for each subunit (.alpha., .beta., and .gamma.) and is activated under conditions of metabolic stress. It is widely expressed in many tissues, including the brain; although, its expression pattern throughout the CNS is unknown. We show that brain mRNA levels for the .alpha.2 and .beta.2 subunits were increased between embryonic days 10 and 14, whereas expression of the .alpha.1, .beta.1, and .gamma.1 subunits was consistent at all ages examd. Immunostaining revealed a mainly neuronal distribution of all isoforms. The .alpha.2 catalytic subunit was highly expressed in neurons and activated astrocytes, whereas the .alpha.1 catalytic subunit showed low expression in neuropil. The .gamma.1 noncatalytic subunit was highly expressed by neurons, but not by astrocytes. Expression of the .beta.1 and .beta.2 noncatalytic subunits varied, but some neurons, such as granule cells of the olfactory bulb, did not express detectable levels of either .beta. isoform. Preferential nuclear localization of the .alpha.2, .beta.1, and .gamma.1 subunits suggests new functions of the AMP- ***activated*** protein kinase, and the ***different*** ***expression*** ***patterns*** and cellular localization between the two catalytic subunits .alpha.1 and .alpha.2 point to different physiol. roles.
OSC.G 78 THERE ARE 78 CAPLUS RECORDS THAT CITE THIS RECORD (79 CITINGS)
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 237 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:188817 CAPLUS <<LOGINID::20100206>>
DN 130:335662
TI The TINS Lecture Understanding the roles of Otx1 and Otx2 in the control of brain morphogenesis
AU Acampora, Dario; Simeone, Antonio
CS International Institute of Genetics and Biophysics, CNR, Naples, 80125, Italy
SO Trends in Neurosciences (1999), 22(3), 116-122 CODEN: TNSCDR; ISSN: 0166-2236
PB Elsevier Science Ltd.
DT Journal; General Review
LA English
AB A review with 49 refs. The murine homologs of the orthodenticle (otd) gene of Drosophila, Otx1 and Otx2, have an important role in brain morphogenesis. Anal. of Otx1 and Otx2 null mice reveals that Otx1 is required primarily for corticogenesis and sense-organ development, while Otx2 is necessary for specification and maintenance of anterior neural plate as well as for proper gastrulation. Cross-phylum recoveries of Otx1 abnormalities by Drosophila otd, and vice versa, indicate that genetic functions required in mammalian-brain development evolved in a primitive ancestor of files and mice. Knock-in mouse models in which Otx2 was replaced with Otx1, and vice versa, provide evidence that the existence of Otx1-/- and Otx2-/- divergent phenotypes largely reflects ***differences*** in ***expression*** ***patterns*** rather than in the biochem. ***activity*** of OTX1 and OTX2. In evolutionary terms, some of these findings lead us to hypothesize a fascinating and crucial role for Otx genes that contributes to the genetic program required for the specification of the development of the vertebrate head.
OSC.G 57 THERE ARE 57 CAPLUS RECORDS THAT CITE THIS RECORD (57 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 238 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:31106 CAPLUS <<LOGINID::20100206>>
DN 130:192684
TI Effect of ploidy and homozygosity on transgene expression in primary tobacco transformants and their androgenetic progenies
AU Beaujean, A.; Sangwan, R. S.; Hodges, M.; Sangwan-Norreel, B. S.
CS Faculte des Sciences Laboratoire Androgenese et Biotechnologie, Universite de Picardie Jules Verne, Amiens, F-80039, Fr.
SO Molecular and General Genetics (1998), 260(4), 362-371
CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB Expression of a transgene is rarely analyzed in the androgenetic progenies of the transgenic plants. Here, the author report differential transgene expression in androgenetic haploid and doubled haploid (DH) tobacco plants as compared to the diploid parental lines, thus demonstrating a gene dosage effect. Using Agrobacterium-mediated transformation, and bacterial reporter genes encoding neomycin phosphotransferase (nptII) and .beta.-glucuronidase (uidA/ GUS), driven resp. by the mas 1' and mas 2' promoters, the authors have generated more than 150 independent transgenic (R0) Nicotiana tabacum plants contg. one or more T-DNA copies. Transgene analyses of these R0, their selfed R1 lines and their corresponding haploid progenies showed an obvious position effect (site of T-DNA insertion on chromosome) on uidA expression. However, transgene (GUS) expression levels were not proportional to transgene copy no. More than 150 haploids and doubled haploids, induced by treatment with colchicine, were produced from 20 independent transgenic R0 plants contg. single and multiple copies of the uidA gene. The authors obsd. that homozygous DH plants expressed GUS at approx. 2.9-fold the level of the corresponding parental haploid plants. This increase in transgene expression may be attributed mainly to the increase (2-fold) in chromosome no. Based on this observation, the authors suggest a strong link between chromosome no. (ploidy dosage effect) and transgene expression. In particular, the authors demonstrate the effect on its expression level of converting the transgene from the heterozygous (in R0 plants) to the homozygous (DH) state: e.g. an increase of 50% was obsd. in the homozygous DH as compared to the original heterozygous diploid plants. The authors propose that ploidy coupled with homozygosity can result in a new type of gene ***activation***

, creating ***differences*** in gene ***expression*** ***patterns*** .
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 239 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:6610 CAPLUS <<LOGINID::20100206>>
DN 130:218796
TI Probing lymphocyte biology by genomic-scale gene expression analysis
AU Alizadeh, Ash; Eisen, Michael; Botstein, David; Brown, Patrick O.; Staudt, Louis M.
CS Metabolism Branch, National Cancer Institute, Bethesda, MD, 20892, USA
SO Journal of Clinical Immunology (1998), 18(6), 373-379
CODEN: JCIMDC; ISSN: 0271-9142
PB Plenum Publishing Corp.
DT Journal; General Review
LA English
AB A review and discussion with 31 refs. The identity and abundance of mRNA species within a cell dictate, to a large extent, the biol. potential of that cell. Although posttranscriptional mechanisms modify protein expression in crit. ways, cellular differentiation requires key changes in gene transcription, as evidenced by the potent phenotypes that result from disruption of transcription factor genes in mice. It is now possible to assess the mRNA profile of a cell globally using recently developed genomics techniques. This review focuses on the potential of cDNA microarrays to define gene expression in lymphoid cells, a field which is in its infancy. Examples of cellular activation genes and cytokine inducible genes discovered using this technol. are presented but these represent only a taste of the fruit that this new technol. will ultimately bear. Gene ***expression*** ***profiles*** should provide essential new insights into lymphocyte ***differentiation*** and ***activation*** , the pathogenesis of immune disorders, and the mol. abnormalities in lymphoid malignancies.
OSC.G 74 THERE ARE 74 CAPLUS RECORDS THAT CITE THIS RECORD (74 CITINGS)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 240 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:754405 CAPLUS <<LOGINID::20100206>>
DN 130:92501
TI Stress-activated signalling pathways in yeast
AU Toone, W. Mark; Jones, Nic
CS Imperial Cancer Research Fund, London, WC2A 3PX, UK
SO Genes to Cells (1998), 3(8), 485-498 CODEN: GECELL; ISSN: 1356-9597
PB Blackwell Science Ltd.
DT Journal; General Review
LA English
AB A review with 91 refs. Eukaryotic cells have developed response mechanisms to combat the harmful effects of a variety of stress conditions. In the majority of cases, such responses involve ***changes*** in the gene ***expression*** ***pattern*** of the cell, leading to increased levels and ***activities*** of proteins that have stress-protective functions. Over the last few years, considerable progress has been made in understanding how stress-dependent transcriptional changes are brought about, and it transpires that the underlying mechanisms are highly conserved, being similar in organisms ranging from yeast to man. Many of the stress signals derive from the extracellular environment and accordingly these signals require transduction from the cell surface to the nucleus. This is accomplished through stress-activated signalling pathways, key amongst which are the highly conserved stress-activated MAP kinase pathways. Stimulation of these pathways leads to the increased activity of specific transcription factors and consequently the increased expression of certain stress-related genes. In this review, we focus on the progress that has been made in understanding these stress responses in yeast.
OSC.G 70 THERE ARE 70 CAPLUS RECORDS THAT CITE THIS RECORD (70 CITINGS)
RE.CNT 92 THERE ARE 92 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 241 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:740343 CAPLUS <<LOGINID::20100206>>
DN 130:137472
TI Differentiation of EL4 lymphoma cells by tumoral environment is associated with inappropriate expression of the large chondroitin sulfate proteoglycan PG-M and the tumor-associated antigen HTgp-175
AU Rottiers, Pieter; Verfaillie, Tine; Contreras, Roland; Revets, Hilde; Desmedt, Marjory; Dooms, Hans; Fiers, Walter; Grooten, Johan
CS Department of Molecular Biology, Molecular Immunology Unit, Flanders Interuniversity Institute for Biotechnology, University of Ghent, Ghent, Belg.
SO International Journal of Cancer (1998), 78(4), 503-510
CODEN: IJCNAW; ISSN: 0020-7136
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Progression to malignancy of transformed cells involves complex genetic alterations and aberrant gene expression patterns. Whereas aberrant gene expression is often caused by alterations in individual genes, the contribution of the tumoral environment to the triggering of this gene expression is less well-established. The stable but heterogeneous expression in cultured EL4/13 cells of a novel tumor-assocd. antigen, designated as HTgp-175, was chosen for the investigation of gene expression during tumor formation. Homogeneously HTgp-175-neg. EL4/13 cells, isolated by cell sorting or obtained by subcloning, acquired HTgp-175 expression as a result of tumor formation. The tumorigenicity of HTgp-175-neg. vs. HTgp-175-pos. EL4 variants was identical, indicating that induction, but not selection, accounted for the phenotypic switch from HTgp-175-neg. to HTgp-175-pos. Although mutagenesis expts. showed that the protein was not essential for tumor establishment, tumor-derived cells showed increased malignancy, linking HTgp-175 expression with genetic changes accompanying tumor progression. This novel gene expression was not an isolated event, since it was accompanied by ectopic expression of the large chondroitin sulfate proteoglycan PG-M and of normal differentiation antigens. Thus, signals derived from the tumoral microenvironment contribute to the aberrant gene ***expression*** ***pattern*** of malignant cells, apparently by fortuitous ***activation*** of ***differentiation*** processes and cause expression of novel differentiation antigens as well as of inappropriate tumor-assocd. and ectopic antigens.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 242 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:711822 CAPLUS <<LOGINID::20100206>>
DN 130:107901
TI A Rap guanine nucleotide exchange factor enriched highly in the basal ganglia
AU Kawasaki, Hiroaki; Sprinett, Gregory M.; Toki, Shinichiro; Canales, Juan J.; Harlan, Patricia; Blumenstiel, Justin P.; Chen, Emy J.; Bany, I. Amy; Mochizuki, Naoki; Ashbacher, Amy; Matsuda, Michiyuki; Housman, David E.; Graybiel, Ann M.
CS Department of Brain and Cognitive Sciences and Center for Cancer Research, Department of Biology, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(22), 13278-13283 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Ras proteins, key regulators of growth, differentiation, and malignant transformation, recently have been implicated in synaptic function and region-specific learning and memory functions in the brain. Rap proteins, members of the Ras small G protein superfamily, can inhibit Ras signaling through the Ras/Raf-1/mitogen-activated protein (MAP) kinase pathway or, through B-Raf, can activate MAP kinase. Rap and Ras proteins both can be activated through guanine nucleotide exchange factors (GEFs). Many Ras GEFs, but to date only one Rap GEF, have been identified. The authors now report the cloning of a brain-enriched gene, CalDAG-GEFI, which has substrate specificity for Rap1A, dual binding domains for calcium (Ca2+) and diacylglycerol (DAG), and enriched expression in brain basal ganglia pathways and their axon-terminal regions. Expression of CalDAG-GEFI activates Rap1A and inhibits Ras-dependent activation of the Erk/MAP kinase cascade in 293T cells. Ca2+ ionophore and phorbol ester strongly and additively enhance this Rap1A activation. By contrast, CalDAG-GEFII, a second CalDAG-GEF family member that the authors cloned and found identical to RasGRP, exhibits a ***different*** brain ***expression*** ***pattern*** and fails to ***activate*** Rap1A, but ***activates*** H-Ras, R-Ras, and the Erk/MAP kinase cascade under Ca2+ and DAG modulation. The authors propose that CalDAG-GEF proteins have a crit. neuronal function in detg. the relative activation of Ras and Rap1 signaling induced by Ca2+ and DAG mobilization. The expression of CalDAG-GEFI and CalDAG-GEFII in hematopoietic organs suggests that such control may have broad significance in Ras/Rap regulation of normal and malignant states.
OSC.G 214 THERE ARE 214 CAPLUS RECORDS THAT CITE THIS RECORD (214 CITINGS)
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 243 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:646154 CAPLUS <<LOGINID::20100206>>
DN 129:341973
OREF 129:69625a,69628a
TI Functional redundancy of the nuclear factor .kappa.B inhibitors I.kappa.B.alpha. and I.kappa.B.beta.
AU Cheng, Janet D.; Ryseck, Rolf-Peter; Attar, Ricardo M.; Dambach, Donna; Bravo, Rodrigo
CS Department of Oncology, Bristol-Myers Squibb Pharmaceutical Research Institute, Princeton, NJ, 08543-4000, USA
SO Journal of Experimental Medicine (1998), 188(6), 1055-1062 CODEN: JEMEAV; ISSN: 0022-1007
PB Rockefeller University Press
DT Journal
LA English
AB The transcription factor NF-.kappa.B is sequestered in the cytoplasm by the inhibitor proteins of the I.kappa.B family. Each member of the I.kappa.B exhibits structural and biochem. similarities as well as differences. In an effort to address the functional redundancy of two closely related I.kappa.B mols., I.kappa.B.alpha. and I.kappa.B.beta., we generated knock-in mice by replacing the I.kappa.B.alpha. gene with the I.kappa.B.beta. gene. The knock-in mice do not express I.kappa.B.alpha., but express a T7-tagged I.kappa.B.beta. under the promoter and regulatory sequence of ikba. Unlike the I.kappa.B.alpha.-deficient mice, which display severe postnatal developmental defects and die by postnatal day 8, homozygous knock-in mice survive to adulthood, are fertile, and exhibit no apparent abnormalities. Furthermore, thymocytes and embryonic fibroblasts from the knock-in animals exhibit an inducible NF-.kappa.B response similar to that of wild-type animals. These results indicate that I.kappa.B.alpha. and I.kappa.B.beta. share significant similarities in their biochem. ***activity*** , and that they acquired their ***different*** functions from divergent ***expression*** ***patterns*** during evolution.
OSC.G 55 THERE ARE 55 CAPLUS RECORDS THAT CITE THIS RECORD (56 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 244 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:635854 CAPLUS <<LOGINID::20100206>>
DN 129:227038
OREF 129:46069a,46072a
TI Proteome and proteomics. New technologies, new concepts, and new words
AU Anderson, N. Leigh; Anderson, Norman G.
CS Large Scale Biology Corporation, Rockville, MD, 20850, USA
SO Electrophoresis (1998), 19(11), 1853-1861 CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH Verlag GmbH
DT Journal; General Review
LA English
AB A review with 41 refs. The goal of ***proteomics*** is a comprehensive, quant. description of protein expression and its ***changes*** under the influence of biol. perturbations such as disease or ***drug*** treatment. Quant. anal. of protein expression data obtained by high-throughput methods has led us to define the concept of regulatory homol. and use it to begin to elucidate the basic structure of gene expression control in vivo. Such investigations lay the groundwork for construction of comprehensive databases of mechanisms (cataloguing possible biol. outcomes), the next logical step after the soon to be completed cataloguing of genes and gene products. Mechanism databases provide a roadmap towards effective therapeutic

intervention that is more direct than that offered by conventional genomics approaches.
OSC.G 353 THERE ARE 353 CAPLUS RECORDS THAT CITE THIS RECORD (355 CITINGS)

L12 ANSWER 245 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:629220 CAPLUS <<LOGINID::20100206>>
DN 130:64414
TI Study on MDM2 and p53 gene proteins expression on acute leukemic cells and its correlation with chemotherapeutic efficacy
AU Lin, Maofang; Liu, Yanchun; Jin, Jie
CS First Affiliated Hospital, Zhejiang Medical University, Hangzhou, 310003, Peop. Rep. China
SO Zhonghua Xueyexue Zazhi (1998), 19(7), 350-352 CODEN: CHTCD7; ISSN: 0253-2727
PB Zhongguo Yixue Kexueyuan Xueyexue Yanjiuso
DT Journal
LA Chinese
AB MDM2 and p53 gene proteins expression was assayed by immunohistochem. staining to explore MDM2 and p53 gene proteins expression on human acute leukemia (AL) cells and their predictive value for chemotherapeutic efficacy. The expression rates of MDM2 and p53 gene proteins were 71.7% and 21.7% resp. in 46 AL patients. The rates were slightly higher in relapse/refractory AL than in previously untreated AL; there was no difference among AL subtypes. MDM2+ and p53- accounted for 67.4%, while the uniform expression of MDM2 and p53 15.2% ($P < 0.01$). The marrow complete remission (CR) rate (69.2%) of MDM2- patients was higher than that (33.3%) of MDM2+ patients ($P < 0.05$). Two of patients with MDM2+++ gained CR and then MDM2 turned neg. MDM2 gene protein was neg. related with p53 gene protein in AL cells. ***Different*** ***expression*** ***patterns*** of the two gene proteins could influence the ***therapeutic*** efficacy, and combined detection of the two may be used as a prognostic parameter for AL patients.

L12 ANSWER 246 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:616559 CAPLUS <<LOGINID::20100206>>
DN 130:36835
TI Matrix metalloproteinases MMP-2 and MMP-9 in denervated muscle and injured nerve
AU Kherif, S.; Dehaupas, M.; Lafuma, C.; Fardeau, M.; Alameddine, H. S.
CS INSERM U 153, Developpement, Pathologie, Regeneration du Systeme Neuromusculaire, Institut de Myologie, Hopital de la Pitie-Salpetriere, Paris, FR-75651, Fr.
SO Neuropathology and Applied Neurobiology (1998), 24(4), 309-319 CODEN: NANEDL; ISSN: 0305-1846
PB Blackwell Science Ltd.
DT Journal
LA English
AB Nerve crush or axotomy results in a transient or longterm denervation accompanied by remodelling in nerve, muscle and neuromuscular junctions. These changes include an increased turnover of several extracellular matrix mols. and proliferation of Schwann cells in injured nerves. Given the role of matrix degrading metalloproteinases MMP-2 and MMP-9 (gelatinases-type IV collagenases) in extracellular matrix remodelling, the authors investigated their regulation and activation in denervated muscles and injured nerves in mice. For this, immunofluorescence using MMP-2 and MMP-9 antibodies was carried concomitantly with gelatin zymog. and quantification of gelatinase activity using [3H]-gelatin substrate. Results show that in normal mouse muscles MMP-2 and MMP-9 are localized at the neuromuscular junctions, in Schwann cells and the perineurium of the i.m. nerves. In denervated mouse muscles, MMP-2 immunolabeling persists at the neuromuscular junctions but decreases in the nerves whereas MMP-9 immunolabeling persists at the neuromuscular junctions but is enhanced in degenerated i.m. nerves. Denervated muscles did not show any significant ***change*** of gelatinolytic ***activity*** or ***expression*** ***pattern*** while injured nerves exhibited a transient increase of MMP-9 and activation of MMP-2. In conclusion, this study demonstrates that MMP-2 and MMP-9 are expressed at mouse neuromuscular junctions and that their localization and expression pattern appear not to be modified by denervation. Their modulation in injured nerves suggests they are involved in axonal degeneration and regeneration.
OSC.G 40 THERE ARE 40 CAPLUS RECORDS THAT CITE THIS RECORD (40 CITINGS)
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 247 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:578373 CAPLUS <<LOGINID::20100206>>
DN 129:326597
OREF 129:66483a,66486a
TI From genome to proteome
AU Noguchi, Teruhisa
CS Helix Research Institute, Inc., Chiba, Japan
SO Yakubutsu Dotai (1998), 13(3), 268-272 CODEN: YADOEL; ISSN: 0916-1139
PB Nippon Yakubutsu Dotai Gakkai
DT Journal; General Review
LA Japanese
AB A review without ref. on clin. applications of mol. genetics, the genome of Helicobacter pylori, bioinformatics, and mol. genetic study of proteomes. The ***proteome*** is the protein expression and its ***changes*** under the influence of biol. perturbations such as disease or ***drug*** treatment.

L12 ANSWER 248 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:571752 CAPLUS <<LOGINID::20100206>>
DN 129:313447
OREF 129:63909a,63912a
TI Cellulase activity and gene expression in citrus fruit abscission zones during and after ethylene treatment
AU Kazokas, William C.; Burns, Jacqueline K.
CS Citrus Research and Education Center, University of Florida, Lake Alfred, FL, 33850, USA
SO Journal of the American Society for Horticultural Science (1998), 123(5), 781-786 CODEN: JOSHB5; ISSN: 0003-1062
PB American Society for Horticultural Science
DT Journal
LA English
AB Mature and immature "Valencia" orange [Citrus sinensis (L.) Osbeck] and immature "Valencia" orange and "Tahiti" lime (Citrus latifolia Tan.) fruit with attached pedicels were treated with 8 .mu.L/L ethdot L-1 ethylene for periods up to 24 h. Endo-.beta.-1,4-glucanase (cellulase) activity and gene expression were detd. in fruit abscission zones during and after ethylene exposure. Cellulase activities were not detected in mature "Valencia" orange and immature "Tahiti" lime fruit abscission zones immediately following harvest and after 6 h of ethylene treatment. After 12 h of ethylene treatment, cellulase activity increased and was

highest after 24 h. Cellulase gene expression preceded the rise in cellulase activity and was detectable after 6 h of ethylene treatment, but then declined after 12 h. Following transfer to air storage, abscission zone cellulase activity in mature "Valencia" fruit remained high, whereas activity in immature "Tahiti" fruit declined. After 168 h air storage, activity in abscission zones of mature "Valencia" fruit decreased slightly, but activity in abscission zones of immature "Tahiti" lime fruit increased to the highest level. Expression of abscission zone cellulase gene Cel-a1 in abscission zones of mature "Valencia" fruit markedly increased after transfer to air and was highest after 48 h air storage. Cel-a1 expression returned to low levels after 168 h of air storage, but expression of cellulase gene Cel-b1 remained at low levels throughout the air storage period. Expression of Cel-a1 and Cel-b1 declined in fruit abscission zones of immature "Valencia" and "Tahiti" lime fruit upon transfer to air. After 168 h of air storage, expression of Cel-a1 again rose to high levels but Cel-b1 remained low. The results suggest that ***differences*** in cellulase ***activity*** , and gene ***expression*** ***measured*** in mature and immature fruit abscission zones during ethylene treatment and subsequent air storage may, in part, explain the differential response of mature and immature fruit to abscission agents.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 249 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:547265 CAPLUS <<LOGINID::20100206>>
DN 129:326720
OREF 129:66507a,66510a
TI Fork head domain genes in zebrafish
AU Odenthal, Jorg; Nusslein-Volhard, Christiane
CS MPI fur Entwicklungsbiologie, Tubingen, D-72076, Germany
SO Development Genes and Evolution (1998), 208(5), 245-258
CODEN: DGEVFT; ISSN: 0949-944X
PB Springer-Verlag
DT Journal
LA English
AB Nine members of the fork head domain gene family (fkd1-fkd9) were isolated from early cDNA libraries in the zebrafish. They show unique expression patterns in whole-mount RNA in situ hybridization during the first 24 h of embryonic development. These fkd genes fall into three of ten classes, based on sequence similarities within the DNA-binding domain, whereas members for the other seven classes described in other vertebrates were not found. In addn. to conserved residues at certain positions in the fork head domain, characteristic transcription ***activation*** domains as well as similarities in ***expression*** ***patterns*** were found for members of the ***different*** classes. Members of class I (fkd1/axial, fkd2/Zffkh1, fkd4 and Jkd7) are differentially transcribed in unsegmented dorsal axial structures such as the floor plate, the notochord, the hypochord and, in addn., the endoderm. Transcripts of fkd3 and fkd5 (class II) are mainly detected in the cells of the ectoderm which form neural tissues, as is the case for genes of this class in other species. RNAs of the three members of class V (fkd6, fkd8 and fkd9) are expressed in the paraxial mesoderm and transiently in the neuroectoderm. Gene fkd6 is strongly expressed in neural crest cells from early stages on, whereas fkd2 and fkd7 are transcribed in individual neural crest cells in the pharyngula period.
OSC.G 239 THERE ARE 239 CAPLUS RECORDS THAT CITE THIS RECORD (239 CITINGS)
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 250 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:541858 CAPLUS <<LOGINID::20100206>>
DN 129:258103
OREF 129:52531a
TI Expression profile of active genes in granulocytes
AU Itoh, Koichi; Okubo, Kousaku; Utiyama, Hiroyasu; Hirano, Tetsuo; Yoshii, Junji; Matsubara, Kenichi
CS Institute for Molecular and Cellular Biology, Osaka University, Suita, Japan
SO Blood (1998), 92(4), 1432-1441 CODEN: BLOOAW; ISSN: 0006-4971
PB W. B. Saunders Co.
DT Journal
LA English
AB A no. of genes active in granulocytes have been intensively studied as to the function of their products and their expression controls. However, the intensities and relative order of these gene activities have not been studied. This report describes an ***expression*** ***profile*** of 748 ***different*** species of ***active*** genes in human peripheral granulocytes obtained by analyzing a 3'-directed cDNA library that faithfully represents the mRNA population in the source cells. A significant fraction (20.3% of the total) of the expressed genes in granulocytes consisted of nuclear proteins such as DNA binding proteins, of secretory proteins such as cytokines, and of membrane proteins such as major histocompatibility complex (MHC) proteins and receptors. By comparing this expression profile with 11 profiles similarly obtained with unrelated human cells/tissues, we discovered 10 novel genes that are likely to act specifically in granulocytes. Comparison of this expression profile with that obtained with granulocytoids widely used as a granulocyte model by inducing a cultured promyelocytic leukemia cell line HL60 showed similarities and dissimilarities of gene expressions.
OSC.G 49 THERE ARE 49 CAPLUS RECORDS THAT CITE THIS RECORD (50 CITINGS)
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 251 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:454568 CAPLUS <<LOGINID::20100206>>
DN 129:214972
OREF 129:43667a,43670a
TI Detection of transcripts initiated from two viral promoters (Cp and Wp) in Epstein-Barr virus-infected nasopharyngeal carcinoma cells and biopsies
AU Chang, Yao; Sheen, Tzung-Shiahn; Lu, Jean; Huang, Yu-Tzu; Chen, Jen-Yang; Yang, Czau-Siung; Tsai, Ching-Hwa
CS Graduate Institute of Microbiology, College of Medicine, National Taiwan University, Taipei, Taiwan
SO Laboratory Investigation (1998), 78(6), 715-726 CODEN: LAINAW; ISSN: 0023-6837
PB Williams & Wilkins
DT Journal
LA English
AB ***Different*** ***activation*** of Epstein-Barr virus (EBV) promoters results in distinct ***expression***

patterns of EBV nuclear antigens (EBNAs) and may further decide the role of EBV in the cellular pathogenesis. In EBV-assocd. nasopharyngeal carcinoma (NPC) biopsies, it has generally been believed that Q promoter (Qp)-initiated EBNA1 is the only EBNA gene to be expressed and that the other two viral promoters, Cp and Wp, which can lead to expression of EBNA1-6, are inactive. However, the failure to demonstrate the activities of Cp and Wp may have been due to the limited sensitivities of detection approaches used. In the present article, the EBV promoter usage and gene expression were re-examd. in both EBV-infected NPC cells in vitro and NPC biopsies in vivo. An NPC cell line susceptible to EBV infection in vitro was established by transfection with a plasmid expressing a well-known EBV receptor, CR2. The presence of viral DNA and EBNA proteins was demonstrated in these EBV-infected cells using PCR and anticomplement immunofluorescence assay, resp. As has been identified in NPC biopsies, viral transcripts of Qp-initiated EBNA1, latent membrane protein (LMP)1, LMP2A, LMP2B, and BamHI A genes, as well as the EBV-encoded small RNA (EBER)1 were detected in these in vitro-infected cells using reverse-transcription-PCR. Notably, viral transcripts initiated from Cp or Wp were also found in the infected cells. Furthermore, Cp- or Wp-initiated transcripts and EBNA2 mRNA were detected in some NPC biopsies. Taking advantage of this sensitive detection approach, the authors' observation that Cp and Wp may be active in NPC cells raises the possibility that EBNA2 to 6, in addn. to EBNA1, may play roles in the pathogenesis of NPC.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 252 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:438127 CAPLUS <<LOGINID::20100206>>
DN 129:158224
OREF 129:32149a,32152a
TI Nitric oxide synthases: catalytic function and progress towards selective inhibition
AU Mayer, B.; Andrew, Penelope
CS Institut fur Pharmakologie und Toxikologie, Karl-Franzens-Universitat Graz, Universitatsplatz 2, Graz, A-8010, Austria
SO Naunyn-Schmiedeberg's Archives of Pharmacology (1998), 358(1), 127-133 CODEN: NSAPDC; ISSN: 0028-1298
PB Springer-Verlag
DT Journal; General Review
LA English
AB A review with 69 refs. Biosynthesis of nitric oxide (NO) is performed by the dimeric, heme-contg. enzyme nitric oxide synthase, which requires the flavins FAD and FMN, as well as the pteridine cofactor (6R)-5,6,7,8-tetrahydro-L-biopterin (H4biopterin) in order to catalyze the NADPH-dependent oxidn. of L-arginine. The three major isoforms of nitric oxide synthase (NOS), although identical in that they contain a carboxy-terminal reductase and an amino-terminal oxygenase domain, fulfill diverse physiol. functions, according to their ***differing*** ***expression*** ***patterns*** and mechanisms of ***activation*** . The pteridine H4biopterin, which affects both the conformational stability and activity of NOS, demonstrates anticooperative binding which results in the stoichiometric prodn. of NO and O2-. Physiol. mechanisms involving superoxide dismutase and reduced glutathione exist to avoid the subsequent formation of the potent oxidant peroxynitrite. With regard to inhibition of NO prodn., novel isoform-selective inhibitors are proving useful not only for dissecting the physiol. functions of NOS, but also in the development of novel therapeutic agents.
OSC.G 58 THERE ARE 58 CAPLUS RECORDS THAT CITE THIS RECORD (58 CITINGS)
RE.CNT 69 THERE ARE 69 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 253 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:414289 CAPLUS <<LOGINID::20100206>>
DN 129:147985
OREF 129:30171a
TI Direct visualization of antigen-specific T cells: HTLV-1 Tax11-19-specific CD8+ T cells are activated in peripheral blood and accumulate in cerebrospinal fluid from HAM/TSP patients
AU Greten, Tim F.; Slansky, Jill E.; Kubota, Ryuji; Soldan, Samantha S.; Jaffee, Elizabeth M.; Leist, Thomas P.; Pardoll, Drew M.; Jacobson, Steven; Schneck, Jonathan P.
CS Department of Oncology and Pathology, Johns Hopkins University School of Medicine, Baltimore, MD, 21205, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(13), 7568-7573 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Human T lymphotropic virus type 1 (HTLV-1) -assocd. myelopathy/tropic spastic paraparesis is a demyelinating inflammatory neurol. disease assocd. with HTLV-1 infection. HTLV-1 Tax11-19-specific cytotoxic T cells have been isolated from HLA-A2-pos. patients. We have used a peptide-loaded sol. HLA-A2-Ig complex to directly visualize HTLV-1 Tax11-19-specific T cells from peripheral blood and cerebrospinal fluid without in vitro stimulation. Five of six HTLV-1-assocd. myelopathy/tropic spastic paraparesis patients carried a significant no. (up to 13.87%) of CD8+ lymphocytes specific for the HTLV-1 Tax11-19 peptide in their peripheral blood, which were not found in healthy controls. Simultaneous comparison of peripheral blood and cerebrospinal fluid from one patient revealed 2.5-fold more Tax11-19-specific T cells in the cerebrospinal fluid (23.7% vs. 9.4% in peripheral blood lymphocyte). Tax11-19-specific T cells were seen consistently over a 9-yr time course in one patient as far as 19 yrs after the onset of din. symptoms. Further anal. of HTLV-1 Tax11-19-specific CD8+ T lymphocytes in HAM/TSP patients showed ***different*** ***expression*** ***patterns*** of ***activation*** markers, intracellular TNF-.alpha. and .gamma.-interferon depending on the severity of the disease. Thus, visualization of antigen-specific T cells demonstrates that HTLV-1 Tax11-19-specific CD8+ T cells are activated, persist during the chronic phase of the disease, and accumulate in cerebrospinal fluid, showing their pivotal role in the pathogenesis of this neurol. disease.
OSC.G 128 THERE ARE 128 CAPLUS RECORDS THAT CITE THIS RECORD (128 CITINGS)
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 254 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:369155 CAPLUS <<LOGINID::20100206>>
DN 129:134371
OREF 129:27453a,27456a

TI Different expression of prostaglandin-H synthase isoenzymes and lipoxygenases during multistage carcinogenesis in mouse skin
AU Furstenberger, G.; Muller-Decker, K.; Scholz, K.; Loschke, M.; Lehmann, W. D.; Marks, F.
CS Research Program Tumor Cell Regulation, German Cancer Research Center, Heidelberg, 69120, Germany
SO Advances in Experimental Medicine and Biology (1997), 400A(Eicosanoids and Other Bioactive Lipids in Cancer, Inflammation, and Radiation Injury 2, Pt. A), 419-424 CODEN: AEMBAP; ISSN: 0065-2598
PB Plenum Publishing Corp.
DT Journal
LA English
AB The authors present evidence that prostaglandin-H synthase (PGHS)-1 and PGHS-2 are differentially regulated at the mRNA and protein level in normal, transiently and chronically hyperplastic and neoplastic epidermis. The epidermal 8- and 12-lipoxygenase ***activities*** also showed a ***different*** ***expression*** ***pattern***
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 255 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:350681 CAPLUS <<LOGINID::20100206>>
DN 129:79604
OREF 129:16400h,16401a
TI Differential expression of peroxisome proliferator-activated receptor-.alpha., -.beta., and -.gamma. during rat embryonic development
AU Braissant, Olivier; Wahli, Walter
CS Institut de Biologie Animale, Universite de Lausanne, Lausanne, 1015, Switz.
SO Endocrinology (1998), 139(6), 2748-2754 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB The ***expression*** ***patterns*** of the three ***different*** peroxisome proliferator- ***activated*** receptor (PPAR) isotypes have been detd. during rat embryonic development by in situ hybridization. The expression of PPAR.alpha. starts late in development, with increasing levels in organs such as liver, kidney, intestine, and pancreas, in which it will also be present later in adulthood to regulate its specific target genes. PPAR.alpha. is also transiently expressed in the embryonic epidermis and central nervous system. PPAR.gamma. presents a very restricted pattern of expression, being strongly expressed in brown adipose tissue, in which differentiation has been shown to participate. Like PPAR.alpha., it is also expressed transiently in the central nervous system. Interestingly, PPAR.alpha.-, -.beta. and -.gamma. are coexpressed at high levels in brown adipose tissue. Finally, the high and ubiquitous expression of PPAR.beta. suggests some fundamental role(s) that this receptor might play throughout development.
OSC.G 239 THERE ARE 239 CAPLUS RECORDS THAT CITE THIS RECORD (239 CITINGS)
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 256 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:32694 CAPLUS <<LOGINID::20100206>>
DN 128:176493
OREF 128:34695a,34698a
TI Identification of candidate genes for drug discovery by differential display
AU Shiue, Lily
CS Millennium Pharmaceuticals, Cambridge, MA, USA
SO Drug Development Research (1997), 41(3/4), 142-159 CODEN: DDREDK; ISSN: 0272-4391
PB Wiley-Liss, Inc.
DT Journal; General Review
LA English
AB A review, with 95 refs. Regulation of gene expression can specify cellular fate, define responses to stimuli, and contribute to complex microenvironments present in tissues. Identification of differentially expressed genes in exptl. paradigms can help elucidate underlying biochem. pathways and thus reveal potential therapeutic targets. The technique of differential display uses arbitrarily primed PCR to sample complex cDNA populations of interest; amplified portions of mRNAs are analyzed by denaturing gel electrophoresis and those which are differentially represented can be directly visualized and cloned. PCR-based techniques for anal. of gene expression are reliable and extremely sensitive. In comparison to traditional methods, such as subtractive hybridization, differential display allows for many samples to be compared in parallel, and the requirement for starting material is low. There are a plethora of examples in the literature of how differentially expressed genes can be rapidly identified in exptl. paradigms ranging from cells treated in culture to whole organs of treated animals. The challenge for the researcher is then defining candidate genes for ***drug*** discovery from an initial screen based only on ***differential*** ***expression*** ***patterns*** . Careful exptl. design and execution are crit. for optimal use of such methodologies to fill a gene discovery pipeline. In this article, the merits and potential pitfalls of differential display and related PCR-based techniques are discussed. Current protocols are reviewed and innovations pertaining to high-through-put applications are noted.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 105 THERE ARE 105 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 257 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:793719 CAPLUS <<LOGINID::20100206>>
DN 128:98392
OREF 128:19157a,19160a
TI The arginine deiminase pathway in Rhizobium etli: DNA sequence analysis and functional study of the arcABC genes
AU D'Hooghe, Inge; Vander Wauven, Corinne; Michiels, Jan; Tricot, Catherine; De Wilde, Petra; Vanderleyden, Jos; Stalon, Victor
CS F. A. Janssens Laboratory of Genetics, Katholieke Universiteit Leuven, Heverlee, 3001, Belg.
SO Journal of Bacteriology (1997), 179(23), 7403-7409 CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB Sequence anal. upstream of the Rhizobium etli fixLJ homologous genes revealed the presence of three open reading frames homologous to the arcABC genes of Pseudomonas aeruginosa. The P. aeruginosa arcABC genes code for the enzymes of the arginine deiminase pathway: arginine deiminase, catabolic ornithine carbamoyl-transferase (cOTCase), and

carbamate kinase. OTCase activities were measured in free-living R. etli cells and in bacteroids isolated from bean nodules. OTCase activity in free-living cells was obsd. at a different pH optimum than OTCase ***activity*** in bacteroids, suggesting the presence of two enzymes with ***different*** characteristics and different ***expression*** ***patterns*** of the corresponding genes. The characteristics of the OTCase isolated from the bacteroids were studied in further detail and were shown to be similar to the properties of the cOTCase of P. aeruginosa. The enzyme has a pH optimum of 6.8 and a mol. mass of approx. 450 kDa, is characterized by a sigmoidal carbamoyl phosphate satn. curve, and exhibits a cooperativity for carbamoyl phosphate. R. etli arcA mutants, with polar effects on arcB and arcC, were constructed by insertion mutagenesis. Bean nodules induced by arcA mutants were still able to fix nitrogen but showed a significantly lower acetylene redn. activity than nodules induced by the wild type. No significant differences in nodule dry wt., plant dry wt., and no. of nodules were found between the wild type and the mutants. Detn. of the OTCase activity in exts. from bacteroids revealed a strong decrease in activity of this enzyme in the arcA mutant compared to the wild-type strain. Finally, we obsd. that expression of an R. etli arcA-gusA fusion was strongly induced under anaerobic conditions.
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)
RE.CNT 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 258 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:775321 CAPLUS <<LOGINID::20100206>>
DN 128:126331
OREF 128:24751a,24754a
TI Isolation and characterization of mouse high-glycine/tyrosine proteins
AU Aoki, Noriaki; Ito, Kaoru; Ito, Masaaki
CS Department of Dermatology, Niigata University School of Medicine, Niigata, 951, Japan
SO Journal of Biological Chemistry (1997), 272(48), 30512-30518 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB During hair follicle differentiation, several families of keratin proteins are synthesized sequentially. In the present study, cDNA clones encoding six members of mouse high-glycine/tyrosine protein were isolated by screening a cDNA library prepd. from the mouse skin of an anagen phase with a differential hybridization technique. On the basis of their nucleotide and deduced amino acid sequences, they were found to encode two members of high-glycine/tyrosine protein type I and four of type II. Interestingly, one of the four type II proteins had been encoded by two distinct cDNAs. Among the cDNA clones isolated were included the ones encoding a new member of type I and II protein, resp., which possessed an entire open reading frame. Novel type II protein, termed type II.4, with a mol. mass of 15,130 Da was revealed to have significant direct repeats and a cysteine residue at the carboxyl terminus, which indicates that this protein has characteristics intermediate between high-glycine/tyrosine proteins and cysteine-rich proteins. In addn., the new member of type I protein has some features common with type II protein. The authors propose to term this protein type I.alpha. until it is further characterized. Northern blot anal. demonstrated that gene expression of mouse high-glycine/tyrosine proteins followed the hair cycle growth fundamentally and reached its peak at day 9 in the first hair cycle, while two peaks of their expression were obsd. at day 33 and day 39 in the second cycle. Their transcripts were expressed in the cortical cells of hair follicles but not in the cells of the outer root sheath, inner root sheath, or medulla. Moreover, their gene expression commenced at different levels in cortical cells. The novel findings that each gene is ***activated*** transcriptionally with a distinct ***expression*** ***pattern*** spatially and temporally suggest that there is a remarkable ***difference*** in the distribution of these proteins in hair.
OSC.G 18 THERE ARE 18 CAPLUS RECORDS THAT CITE THIS RECORD (18 CITINGS)
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 259 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:741491 CAPLUS <<LOGINID::20100206>>
DN 128:46013
OREF 128:8983a,8986a
TI Markers of vertebrate mesoderm induction
AU Stennard, Fiona; Ryan, Kenneth; Gurdon, J. B.
CS Wellcome/CRC Institute, Cambridge, CB2 1QR, UK
SO Current Opinion in Genetics & Development (1997), 7(5), 620-627 CODEN: COGDET; ISSN: 0959-437X
PB Current Biology Ltd.
DT Journal; General Review
LA English
AB A review, with 79 refs. Mesoderm formation is the 1st major differentiative event in vertebrate development. Many new mesoderm-specific genes have recently been described in the mouse, chick, frog, and fish and belong to classes comprising T-domain genes, homeobox genes, and those encoding secreted proteins. The T-domain genes have ***different*** but overlapping ***expression*** ***patterns*** and, in Xenopus, can ectopically ***activate*** nearly all other mesodermal genes. Several new homeobox genes seem to mediate the ventralizing activity of bone morphogenetic protein. New genes encoding secreted proteins induce dorsal mesoderm, in some cases by antagonizing ventralizing factors.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 79 THERE ARE 79 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 260 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:729745 CAPLUS <<LOGINID::20100206>>
DN 128:33352
OREF 128:6541a,6544a
TI Developmental study of hepatic glutamine synthetase in a mouse model of congenital hyperammonemia
AU Skarpetas, Andrew; Mawal, Yogesh; Qureshi, Ijaz A.
CS Department of Pediatrics, Sainte-Justine Hospital, University of Montreal and Pediatric Research Center, Montreal, QC, H3T 1C5, Can.
SO Biochemistry and Molecular Biology International (1997), 43(1), 133-139 CODEN: BMBIES; ISSN: 1039-9712
PB Academic
DT Journal
LA English

AB The development of hepatic glutamine synthetase (GS; EC 6.3.1.2) activity and expression was studied in 1 to 112 day old sparse-fur (spf) mutant mice, with X-linked ornithine transcarbamylase (OTC, EC 2.1.3.3) deficiency. The spf/Y mutant mice were found to have a smaller body wt. yet possessed a larger liver in comparison to normal male mice (+/Y). The neonatal hepatic GS activity was retarded in the spf/Y mice but reached normal values by the 28th day of age, after which it increased as compared to the control CD-1 mice. The spf GS activity remained const. from 28 to 56 days, whereas the CD-1 GS activity decreased. A further significant increase in the spf GS activity was obsd. from 56 day to 112 day indicating its adaptation. The decrease of GS mRNA in the spf/Y mice from 28 to 112 days of age (3.72.+-.0.25 vs 1.68.+-.0.32) suggests translational and post-translational modifications in the regulation of GS activity. The ***changes*** in the ***activity*** and ***expression*** ***patterns*** of GS could be due to an effect of the OTC mutation on the hepatic ammonia metab. This may be indicative of the adaptational processes in the spf mutant mice, which may play a specific role in this animal model to help it to survive with its hyperammonemia.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 261 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:645912 CAPLUS <<LOGINID::20100206>>
DN 127:314484
OREF 127:61401a,61404a
TI Biochemical and antiproliferative properties of 4-[ar(alk)ylamino]pyridopyrimidines, a new chemical class of potent and specific epidermal growth factor receptor tyrosine kinase inhibitor
AU Fry, David W.; Nelson, James M.; Slintak, Veronika; Keller, Paul R.; Rewcastle, Gordon W.; Denny, William A.; Zhou, Hairong; Bridges, Alexander J.
CS Department of Cancer Research, Parke-Davis Pharmaceutical Research, Ann Arbor, MI, 48105, USA
SO Biochemical Pharmacology (1997), 54(8), 877-887 CODEN: BCPCA6; ISSN: 0006-2952
PB Elsevier
DT Journal
LA English
AB The tyrosine kinase inhibitors PD 69896, 153717, and 158780, which belong to the chem. class 4-[ar(alk)ylamino]pyridopyrimidines, have been characterized with respect to enzymol., target specificity, and antiproliferative effects in tumor cells. These compds. were competitive inhibitors with respect to ATP against purified epidermal growth factor (EGF) receptor tyrosine kinase and inhibited EGF receptor autophosphorylation in A431 human epidermoid carcinoma with IC50 values of 2085, 110, and 13 nM, resp. Onset of inhibition was immediate once cells were exposed to these compds., whereas recovery of receptor autophosphorylation activity after the cells were washed free of the compd. was dependent on inhibitory potency. Thus, full activity returned immediately after removal of PD 69896 but required 8 h after exposure to PD 158780. PD 158780 was highly specific for the EGF receptor in Swiss 3T3 fibroblasts, inhibiting EGF-dependent receptor autophosphorylation and thymidine incorporation at low nanomolar concns. while requiring micromolar levels for platelet-derived growth factor- and basic fibroblast growth factor-dependent processes. PD 158780 inhibited heregulin-stimulated phosphorylation in the SK-BR-3 and MDA-MB-453 breast carcinomas with IC50 values of 49 and 52 nM, resp., suggesting that the compd. was active against other members of the EGF receptor family. The antiproliferative effects of this series of compds. against A431 cells correlated precisely with the inhibitory potency against EGF receptor autophosphorylation. PD 158780 reduced clone formation in soft agar of fibroblasts transformed by EGF, EGF receptor, or the neu oncogene but not ras or raf, further demonstrating its high degree of specificity. Finally, this compd. was ***active*** against clone formation in several breast tumors having ***different*** ***expression*** ***patterns*** of the erbB family, indicating an anticancer utility in tumors expressing these receptors.
OSC.G 58 THERE ARE 58 CAPLUS RECORDS THAT CITE THIS RECORD (59 CITINGS)
RE.CNT 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 262 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:644848 CAPLUS <<LOGINID::20100206>>
TI Changing activation sequence in the embryonic chick heart
AU Chuck, Emil T.; Freeman, David M.; Watanabe, Michiko; Rosenbaum, David S.
CS Departments of Pediatrics, Medicine, Biomedical Engineering, and Genetics and the Cardiac Bioelectricity Research and Training Center, Case Western Reserve University, Cleveland, OH, USA
SO Circulation Research (1997), 81(4), 470-476 CODEN: CIRUAL; ISSN: 0009-7330
PB American Heart Association
DT Journal
LA English
AB In the mature heart, impulse propagation through the His-Purkinje system (HPS) is required for efficient ventricular contraction in an apex-to-base direction. However, the embryonic heart begins to contract as a myocardial tube without a specialized conduction system. To identify the developmental stage when the HPS begins to function, we mapped the ventricular depolarization sequence from microvolt-level electrograms recorded from embryonic myocardium using 50-.mu.m extracellular electrodes, high-gain amplification, and signal-processing techniques. Anal. of left ventricular activation in 99 embryonic hearts revealed a transition in the activation sequence that was dependent on developmental stage. As the heart develops, a transition in the activation sequence occurred from the primitive base-to-apex pattern (in 20 of 33 hearts) at early stages (Hamburger-Hamilton stages 25 to 28) to the HPS-like apex-to-base pattern (12 of 17 hearts) late in development (stages 33 to 36). Immunohistol. expts. (n=10) also confirm that the ***expression*** ***pattern*** of two biochem. HPS markers ***changes*** in parallel with the ***change*** to the mature ventricular ***activation*** pattern. These data indicate that the ventricular activation sequence in the chick heart develops to a mature pattern at stages 29 to 31, suggesting that preferential conduction through the HPS begins shortly after ventricular septation is complete.
OSC.G 32 THERE ARE 32 CAPLUS RECORDS THAT CITE THIS RECORD (32 CITINGS)
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 263 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:563259 CAPLUS <<LOGINID::20100206>>
DN 127:189736
OREF 127:36809a,36812a
TI Human antibody engineering using glycosylation-based cytotechnology
AU Tachibana, Hirofumi; Shirahata, Sanetaka
CS Graduate School of Genetic Resources Technology, Kyushu University, Fukuoka, Japan
SO Animal Cell Technology: Basic & Applied Aspects, Proceedings of the Annual Meeting of the Japanese Association for Animal Cell Technology, 8th, Fukuoka, November 6-10, 1995 (1997), Meeting Date 1995, 67-73. Editor(s): Funatsu, Kazumori; Shirai, Yoshihito; Matsushita, Taku. Publisher: Kluwer, Dordrecht, Neth. CODEN: 64WUA2
DT Conference
LA English
AB It has become increasingly clear that the glycosylation of biol. agents is dependent on both the cell type and culture environment of the host cells. Therefore modulating the intracellular and extracellular conditions of the host cells can optimize the glycosylation of biologicals. The technol. involved in this process is called "Glycosylation-Based Cytotechnol.", of which one of its uses is to improve the function of biol. agents by altering the glycosylation pattern of the protein. Using Glycosylation-Based Cytotechnol. we engineered a particular antibody by modulating the carbohydrate structure resulting in an improvement in antigen binding affinity and specificity. Appropriate glycosylation on the light chain, which increased antibody affinity by 20 fold, can be accomplished by modulating monosaccharide availability in the culture medium. Furthermore, if the cell lacks sensitivity to environmental ***change*** for glycosylation ***activity*** , the ***expression*** ***pattern*** of the glycoforms is expected to show little variances regardless of changing culture conditions. Cell clones lacking sensitivity to changes in the availability of glucose for macroheterogeneity of light chain glycosylation were isolated from lectin resistant mutants.

L12 ANSWER 264 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:496914 CAPLUS <<LOGINID::20100206>>
DN 127:203662
OREF 127:39531a,39534a
TI Targeted disruption of the epidermal growth factor receptor impairs growth of squamous papillomas expressing the v-rasHa oncogene but does not block in vitro keratinocyte responses to oncogenic ras
AU Dlugosz, Andrzej A.; Hansen, Laura; Cheng, Christina; Alexander, Natalie; Denning, Mitchell F.; Threadgill, David W.; Magnuson, Terry; Coffey, Robert J., Jr.; Yuspa, Stuart H.
CS Lab. Cellular Carcinogenesis and Tumor Promotion, National Cancer Inst., Bethesda, MD, 20892, USA
SO Cancer Research (1997), 57(15), 3180-3188 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB The authors have assessed the role of epidermal growth factor receptor (EGFR) signaling in biol. responses to the v-rasHa oncogene using primary keratinocytes from Egfr -/- mice and wild-type littermates. On the basis of several criteria, Egfr -/- keratinocytes were unresponsive to either acute or chronic exposure to several EGFR ligands but were stimulated to proliferate in response to several other mitogens. Although conditioned medium from primary keratinocytes transduced with v-rasHa retrovirus (v-rasHa keratinocytes) was a potent mitogen for wild-type but not Egfr -/- keratinocytes, v-rasHa transduction of primary keratinocytes of either genotype resulted in a strong mitogenic response, arguing against an obligatory role for EGFR activation in v-rasHa-mediated stimulation of keratinocyte proliferation. Infection with high-titer v-rasHa retrovirus altered the keratin ***expression*** ***pattern*** in keratinocytes of both genotypes, suppressing ***differentiation*** -specific keratins K1 and K10 while ***activating*** aberrant expression of K8 and K18. In wild-type but not Egfr -/- cultures, K1 and K10 were also suppressed following infection at lower retroviral titers, presumably as a result of paracrine EGFR activation on uninfected cells present in these cultures. Squamous papillomas produced by grafting Egfr -/- v-rasHa keratinocytes onto nude mice were only 21% of the size of wild-type v-rasHa tumors, and a striking redistribution of S-phase cells was detected by immunostaining for bromodeoxyuridine. In Egfr -/- v-rasHa papillomas, the fraction of total labeled nuclei detected in suprabasal layers was increased from 19 to 39%. In contrast, the basal layer labeling index of Egfr -/- papillomas was reduced to 34%, compared to 43% in wild-type tumors. The results indicate that, although autocrine EGFR signaling is not required for keratinocyte responses to oncogenic ras in culture or benign formation in nude mouse grafts, disruption of this pathway impairs growth of v-rasHa papillomas by a mechanism that may involve alterations in keratinocyte cell cycle progression and/or migration in vivo.
OSC.G 48 THERE ARE 48 CAPLUS RECORDS THAT CITE THIS RECORD (48 CITINGS)

L12 ANSWER 265 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:398641 CAPLUS <<LOGINID::20100206>>
DN 127:107816
OREF 127:20771a,20774a
TI Inflammatory cytokines and type I 5'-deiodinase expression in .PHI.1 rat liver cells
AU Davies, Peter H.; Sheppard, Michael C.; Franklyn, Hayne R.
CS Department of Medicine, University of Birmingham, Queen Elizabeth Hospital, Birmingham, B15 2TH, UK
SO Molecular and Cellular Endocrinology (1997), 129(2), 191-198 CODEN: MCENDB; ISSN: 0303-7207
PB Elsevier
DT Journal
LA English
AB Administration of tumor necrosis factor-.alpha. (TNF.alpha.), interleukin-1.beta. (IL-1.beta.), and interleukin-6 (IL-6) to animals and humans results in changes in circulating thyroid hormone concns. similar to those seen in non-thyroidal illness (NTI). Inflammatory cytokines have been postulated as mediators of the euthyroid sick syndrome by inhibiting type 1 5'-deiodinase (5'D-I) enzyme activity. The authors investigated direct effects of cytokines upon 5'D-I ***expression*** , ***measuring*** ***changes*** in 5'D-I enzyme ***activity*** and mRNA in .PHI.1 rat liver cells. All 3 cytokines stimulated 5'D-I enzyme activity: TNF.alpha. 326% (100% in controls), IL-1 297%, and IL-6 272%. Co-incubation with cycloheximide abolished stimulation by each cytokine. Kinetic anal. revealed that stimulation of 5'D-I enzyme activity was a result of increased Vmax, with Km relatively unchanged. The 5'D-I mRNA abundance was not changed following treatment by any of the 3 cytokines. These findings do not support the hypothesis that inflammatory cytokines may mediate the euthyroid sick syndrome by causing inhibition of 5'D-I activity.

OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 266 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:382207 CAPLUS <<LOGINID::20100206>>
DN 127:107066
OREF 127:20591a,20594a
TI Dlx-2 homeobox gene controls neuronal differentiation in primary cultures of developing basal ganglia
AU Ding, Min; Robel, Laurence; James, Alaina J.; Eisenstat, David D.; Leckman, James F.; Rubenstein, John L. R.; Vaccarino, Flora M.
CS Child Study Center, Yale University, New Haven, CT, 06520, USA
SO Journal of Molecular Neuroscience (1997), 8(2), 93-113
CODEN: JMNEES; ISSN: 0895-8696
PB Humana
DT Journal
LA English
AB Homeodomain-contg. genes of the Dlx family are expressed in the developing basal ganglia. To investigate the role of Dlx genes during development, we studied their cellular localization in primary cultures of embryonic basal telencephalon, and examd. the changes in cellular phenotypes resulting from blockade of Dlx-2 expression. Cells contg. Dlx-1, Dlx-2, and Dlx-5 mRNAs are immature cells of the neuronal lineage expressing the microtubule-assocd. proteins (MAPs) MAP1B and MAP2, but not glial fibrillary acidic protein (GFAP). Treatment of these cells with antisense oligonucleotides targeted to Dlx-2 caused a specific decrease of Dlx-2 mRNA and protein. This decrease in the Dlx-2 gene product was assocd. with a decrease in the expression of MAP2, a protein localized in neuronal dendrites, along with a smaller decrease in the 200-kDa neurofilament subunit (NF-H). Proteins expressed preferentially in axons were unchanged. This redn. in MAP2 expression was assocd. with a decrease in dendrite outgrowth and an increased level of cell proliferation. None of these changes were elicited by antisense oligonucleotides targeted to Dlx-1. We suggest that the Dlx-2 gene product regulates two interrelated aspects of neuronal differentiation: the exit from the mitotic cycle and the capability to grow MAP2-pos. dendrites. As such, this gene product may be important for the establishment of neuronal polarity, setting the stage for afferent synaptic connectivity.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)
RE.CNT 67 THERE ARE 67 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 267 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:351902 CAPLUS <<LOGINID::20100206>>
DN 127:76464
OREF 127:14484h,14485a
TI PKC isoenzyme expression and cellular responses to phorbol ester in JEG-3 choriocarcinoma cells
AU Bamberger, Ana-Maria; Bamberger, Christoph M.; Wald, Martin; Jensen, Karen; Schulte, Heinrich M.
CS Institute for Hormone and Fertility Research, University of Hamburg, Hamburg, 22529, Germany
SO Endocrine (1997), 6(2), 111-116 CODEN: EOCRE5; ISSN: 1355-008X
PB Humana
DT Journal
LA English
AB Protein kinase C (PKC) is a key regulatory enzyme involved in the transduction of extracellular growth signals to the cell nucleus. It occurs in several isoforms, the exact functional roles of which have not been established as yet. The tumor-promoting agent 12-O-tetradecanoyl-phorbol acetate (TPA) is the classic activator of PKC and modulates the activity of the activating protein-1 (AP-1) transcription factor complex via this pathway. AP-1, in turn, induces cell proliferation in many tissues. In the present study, the PKC isoenzyme expression pattern in JEG-3 choriocarcinoma cells was analyzed. The results were compared with those obtained in HEC-1B endometrium adenocarcinoma cells, which had previously been characterized in this respect. To gain insight into the possible functional consequences of ***different*** PKC ***expression*** ***patterns** , cell proliferation rates and AP-1 ***activity*** in response to TPA in both cell lines was studied. Western blot anal. of the PKC isoenzyme expression pattern revealed that JEG-3 cells are deficient in the PKC .alpha., .delta., and .epsilon. isoforms. These isoenzymes are strongly expressed in HEC-1B cells, with the .alpha. and .delta. being constitutively active. As opposed to HEC-1B cells, JEG-3 cells did not show an enhanced proliferation rate in response to TPA. Furthermore, TPA-treated JEG-3 cells did not exhibit any change in cell shape and refractory as obsd. in HEC-1B cells. AP-1 activity, as detd. by a transfected AP-1-luciferase reporter plasmid, was induced 10-fold by TPA in JEG-3 cells, yet only threefold in HEC-1B cells. It is concluded from these data that differential expression of a subset of PKCs, e.g., the .alpha., .delta., and .epsilon. isoforms, may serve as an indicator of the proliferative potential in response to growth factors and mitogens. Furthermore, our data indicate that the inducibility of AP-1 activity does not necessarily reflect the proliferative capacity of a given cell type in response to classical tumor promoters such as phorbol ester.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 268 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:339972 CAPLUS <<LOGINID::20100206>>
DN 127:16430
OREF 127:3331a,3334a
TI Effect of HIV-1 gp41 peptide on expression and metabolism of amyloid precursor protein in human astroglioma cell
AU Chong, Young hae; Park, Hae Kyung
CS Department of Microbiology, College of Medicine, Division of Molecular Biology, Ewha Medical Center, Ewha Womans University, Seoul, 158-056, S. Korea
SO Taehan Misaengmul Hakhoechi (1997), 32(2), 245-254
CODEN: TMHCDX; ISSN: 0253-3162
PB Korean Society for Microbiology
DT Journal
LA Korean
AB Significant neurodegeneration leading to neurocognitive disorder and dementia has been obsd. in the central nervous system (CNA) of patients with HIV infection. Part of the neurodegenerative cascade in AIDS dementia may involve glial cells, perhaps through inhibiting the release of glial factors that protect neurons from variety of insults. Here, in an effort to find the mediators of HIV-induced brain damage, the authors examd. the possible effect of a HIV-1 transmembrane protein gp41

peptide (583-599) on expression and metab. of amyloid precursor protein (APP) using human astroglial cell line. RT-PCR anal. demonstrated that gp41 peptide did not ***change*** ***expression*** ***patterns*** of APP mRNAs in lipopolysaccharide (LPS) ***activated*** astroglial cells for 6 h. In contrast, gp41 peptide remarkably downregulated the level of secreted form of APP (sAPP.alpha.), which has been recently demonstrated as a potent neuroprotective factor. The reverse peptide, used as a control had no such effect. The mechanism of gp41 peptide-induced down regulation of sAPP.alpha. prodn. appears to be TGF-.beta. independent. Apparently, gp41 peptide could be one of the mediators involved in the modulation of APP secretion within CNS, possibly contributing to the neuronal degeneration in HIV-1 assocd. neurol. disease.

L12 ANSWER 269 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:253057 CAPLUS <<LOGINID::20100206>>
DN 126:302078
OREF 126:58381a,58384a
TI Transforming growth factor .beta.1-regulated gene expression of Ito cells
AU Knittel, Thomas; Janneck, Thomas; Mueller, Lars; Fellmer, Peter; Ramadori, Giuliano
CS Department of Internal Medicine, Section of Gastroenterology and Endocrinology, University of Gottingen, Gottingen, 37075, Germany
SO Hepatology (Philadelphia) (1996), 24(2), 352-360 CODEN: HPTLD9; ISSN: 0270-9139
PB Saunders
DT Journal
LA English
AB This study analyzed the effects of TGF-.beta.1 on Ito cell activation, proliferation, and on the expression of a set of matrix proteins, antiproteases, and TGF-.beta. receptors both in early cultured and culture-activated Ito cells. Rat liver Ito cells at day 2 of primary culture (early cultured cells) were mainly smooth muscle .alpha.-actin (SMA)-neg., whereas cells at day 6 were judged as activated cells (SMA-pos.). Following 24-h exposure to 1 ng/mL TGF-.beta.1, total protein synthesis, cell proliferation, and expression of the activation marker SMA were not significantly changed. In addn. to previously described stimulatory effects on collagen types I and III, fibronectin, undulin, and proteoglycan-gene expression, TGF-.beta. also dose-dependently increased synthesis and secretion of tenascin, laminin, entactin, collagen type IV, and .alpha.2-macroglobulin, but decreased Cl-esterase inhibitor prodn. by Ito cells, as revealed by immunopptn. of endogenously labeled proteins and by Northern blot anal. The stimulatory effect of TGF-.beta. was evident both in early cultured as well as culture-activated Ito cells. By reverse-transcription PCR anal., TGF-.beta. type II, III, and TGF-.beta./ ***activin*** type I receptors were present in Ito cells, and their ***expression*** ***pattern*** was not ***changed*** upon TGF-.beta. exposure. Northern blot anal. demonstrated that type I TGF-.beta./activin receptor was induced during in vitro activation and that TGF-.beta. exposure resulted in a slight increase of type I and III receptor mRNAs. In summary, the data illustrate that TGF-.beta. is an important fibrogenic mediator acting both on early cultured as well as culture-activated Ito cells, rather than a mitogenic or morphogenic mediator. The differential regulation of TGF-.beta./activin receptors during in vitro activation and their up-regulation by TGF-.beta.1 might represent a mechanism by which the receptor complex regulates TGF-.beta. signaling in Ito cells.
OSC.G 70 THERE ARE 70 CAPLUS RECORDS THAT CITE THIS RECORD (70 CITINGS)

L12 ANSWER 270 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:239041 CAPLUS <<LOGINID::20100206>>
DN 126:312412
OREF 126:60441a,60444a
TI Tissue-specific expression of inhibin/activin subunit and follistatin mRNAs in mid- to late-gestational age human fetal testis and epididymis
AU Roberts, Veronica J.
CS Dep. of Reproductive Medicine, University of California at San Diego, La Jolla, CA, 92093-0674, USA
SO Endocrine (1997), 6(1), 85-90 CODEN: ECORE5; ISSN: 1355-008X
PB Humana
DT Journal
LA English
AB Inhibin/activin subunit (.alpha., .beta.A, and .beta.B) immunoreactive protein localization patterns and cell type specific inhibin .alpha.-subunit mRNA expression have been examd. in early- to midgestational age human fetal testes. The scarcity of available third trimester human fetal tissue has, however, prevented a complete examn. throughout the gestational period and the cell specific expression of follistatin and .beta.A- and .beta.B-subunit mRNAs are currently unknown at any gestational age. In the present study, this gap is filled and report mRNA expression patterns of inhibin/activin subunits in mid- and late-gestational age (21-33 wk) human fetal testes and testicular duct system. We also report the first examn. of follistatin mRNA signals in the human fetal gonad is also reported. Inhibin/actin .alpha.-subunit mRNA signal is present in both tubular and interstitial cells, and .beta.B-subunit mRNA is expressed in seminiferous tubules, in mid- and late-gestational age human fetal testes. Inhibin/activin .beta.A-subunit mRNA was detected in the interstitial cells of remarkably well preserved mid (21 and 22 wk) and late (29 wk) gestational age testis, and is the only activin-system factor mRNA also expressed in tissue of the duct system of the testis (smooth muscle cells of the epididymis). Follistatin mRNA signal was equal to background levels in testicular and dust tissues at all ages examd. These cell specific ***expression*** ***patterns*** suggest prominent and possibly ***differential*** roles for the inhibins and ***activins*** , unopposed by gonadal follistatin, in the human fetal male reproductive system.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)

L12 ANSWER 271 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:225956 CAPLUS <<LOGINID::20100206>>
DN 126:234364
OREF 126:45249a,45252a
TI Expression patterns of the four nuclear factor I genes during mouse embryogenesis indicate a potential role in development
AU Chaudhry, Ali Z.; Lyons, Gary E.; Gronostajski, Richard M.
CS Department of Cancer Biology, Research Institute, Cleveland Clinic Foundation, Cleveland, OH, 44195, USA
SO Developmental Dynamics (1997), 208(3), 313-325 CODEN: DEDYEI; ISSN: 1058-8388
PB Wiley-Liss
DT Journal
LA English
AB The nuclear factor I (NFI) family of site-specific DNA-binding proteins is required for both the cell-type specific transcription of many viral and cellular genes and for the replication of adenovirus DNA. Although binding sites for NFI proteins within

the promoters of several tissue-specific genes have been shown to be essential for their expression, it is unclear which NFI gene products function in specific tissues during development. We have isolated cDNAs from all four murine NFI genes (gene designations Nfia, Nfib, Nfic, and Nfix), assessed the embryonic and postnatal expression patterns of the NFI genes, and detd. the ability of specific NFI proteins to activate transcription from the NFI-dependent mouse mammary tumor virus (MMTV) promoter. In adult mice, all four NFI genes are most highly expressed in lung, liver, heart, and other tissues but only weakly expressed in spleen and testis. The embryonic expression patterns of the NFI genes is complex, with NFI-A transcripts appearing earliest-within 9 days postcoitum in the heart and developing brain. The four genes exhibit unique but overlapping patterns of expression during embryonic development, with high level expression of NFI-A, NFI-B, and NFI-X transcripts in neocortex and extensive expression of the four genes in muscle, connective tissue, liver, and other organ systems. The four NFI gene products studied differ in their ability to activate expression of the NFI-dependent MMTV promoter, with the NFI-B protein being most active and the NFI-A protein being least active. These data are discussed in the context of the developmental expression patterns of known NFI-responsive genes. The ***differential*** ***activation*** of an NFI-dependent promoter, together with the ***expression*** ***patterns*** obsd. for the four genes, indicate that the NFI proteins may play an important role in regulating tissue-specific gene expression during mammalian embryogenesis.
OSC.G 103 THERE ARE 103 CAPLUS RECORDS THAT CITE THIS RECORD (103 CITINGS)

L12 ANSWER 272 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:221949 CAPLUS <<LOGINID::20100206>>
DN 126:291478
OREF 126:56393a
TI Identification, expression pattern and potential activity of Na/Ca exchanger isoforms in rat pancreatic B-cells
AU Van Eylen, F.; Svoboda, M.; Herchuelz, A.
CS Laboratory of Pharmacology, Brussels University School of Medicine, Brussels, Belg.
SO Cell Calcium (1997), 21(3), 185-193 CODEN: CECADV; ISSN: 0143-4160
PB Churchill Livingstone
DT Journal
LA English
AB In the pancreatic B-cell, Na/Ca exchange displays a quite high capacity and participates in the control of cytosolic free Ca2+ concn. The Na/Ca exchanger was recently cloned in various tissues. Two genes coding for two different exchangers (NCX1 and NCX2) have been identified and evidence for several isoforms for NCX1 shown. To characterize the isoform(s) expressed in pancreatic B-cells, a RT-PCR anal. was performed on mRNA from rat pancreatic islets, purified B-cells and insulinoma B-cells (RINm5F cells). PCR amplification did not yield the expected NCX2 DNA fragment but yielded 2 NCX1 bands, corresponding to NaCa3 and NaCa7, in the three prepns. NaCa3 and NaCa7 were equally expressed in pancreatic islets and purified B-cells. In RINm5F cells, NaCa3 expression did not differ from that in islet and purified B-cells but NaCa7 was 3 times less expressed. This lower expression was accompanied by a 3 times lower Na/Ca exchange activity in RINm5F cells compared to islet cells. Our data indicate the existence of 2 NCX1 isoforms but not of NCX2 in pancreatic B-cells. The ***difference*** in both the ***expression*** ***patterns*** of NCX1 isoforms and the ***activity*** of Na/Ca exchange in islet cells and RINm5F cells is compatible with a difference in activity between NaCa3 and NaCa7.
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)

L12 ANSWER 273 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:209556 CAPLUS <<LOGINID::20100206>>
DN 126:261573
OREF 126:50597a,50600a
TI Organ-specific expression of O-acetylserine(thiol)lyase in Arabidopsis thaliana
AU Barroso, Consuelo; Vega, Jose M.; Gotor, Cecilia
CS Institute de Bioquimica Vegetal y Fotosintesis, Facultad de Quimica, CSIC y Universidad de Sevilla, Seville, 41080, Spain
SO Photosynthesis: From Light to Biosphere, Proceedings of the International Photosynthesis Congress, 10th, Montpellier, Fr., Aug. 20-25, 1995 (1995), Volume 3, 619-622. Editor(s): Mathis, Paul. Publisher: Kluwer, Dordrecht, Neth. CODEN: 64DFAW
DT Conference
LA English
AB Expression of the Atcys-3A gene, encoding the cytosolic isoenzyme of O-acetylserine thiol lyase of A. thaliana, was detd. in different organs of mature Arabidopsis by Northern blot anal. The enzyme activity level was also detd. in the various organs of the plant. Organ-specific expression of Atcys-3A transcript was obsd., being most abundant in roots. The enzyme activity level was greatest in stems. There was no correlation between enzyme activity and Atcys-3A mRNA expression in the different plant organs. This is not surprising, since the ***activity*** data reflect the contribution of three ***different*** isoenzymes, whereas the ***expression*** ***pattern*** was only analyzed for the gene encoding the cytosolic isoform.

L12 ANSWER 274 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:592616 CAPLUS <<LOGINID::20100206>>
DN 125:271491
OREF 125:50665a,50668a
TI NeuroD2 and neuroD3: distinct expression patterns and transcriptional activation potentials within the neuroD gene family
AU McCormick, Mary B.; Tamimi, Rulla M.; Snider, Lauren; Asakura, Atsushi; Bergstrom, Donald; Tapscott, S. J.
CS Fred Hutchinson Cancer Research Center, Seattle, WA, 98104, USA
SO Molecular and Cellular Biology (1996), 16(10), 5792-5800 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB The authors have identified two new genes, neuroD2 and neuroD3, on the basis of their similarity to the neurogenic basic-helix-loop-helix (bHLH) gene neuroD. The predicted amino acid sequence of neuroD2 shows a high degree of homol. to neuroD and MATH-2/NEX-1 in the bHLH region, whereas neurod3 is a more distantly related family member. NeuroD3 is expressed transiently during embryonic development, with the highest levels of expression between days 10 and 12. NeuroD2 is initially expressed at embryonic day 11, with persistent expression in the adult nervous system. In situ and Northern (RNA) analyses demonstrate that different regions of the adult nervous system have different relative amts. of neuroD3 and neuroD2 RNA. Similar to neuroD, expression of neuroD2 in developing Xenopus laevis embryos results in ectopic neurogenesis, indicating that neuroD2 mediates neuronal differentiation. Transfection of vectors expressing neuroD3 and neuroD2 into P19 cells shows

that both can activate expression through simple E-box-driven reporter constructs and can activate a reporter driven by the neuroD2 promoter region, but the GAP-43 promoter is preferentially activated by neuroD2. The non-congruent expression pattern and target gene specificity of these highly related neurogenic bHLH proteins make them candidates for conferring specific aspects of the neuronal phenotype.
OSC.G 108 THERE ARE 108 CAPLUS RECORDS THAT CITE THIS RECORD (108 CITINGS)

L12 ANSWER 275 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:541902 CAPLUS <<LOGINID::20100206>>
DN 125:215342
OREF 125:40123a,40126a
TI Characterization of three potato lipoxygenases with distinct enzymic ***activities*** and ***different*** organ-specific and wound-regulated ***expression*** ***patterns***
AU Royo, Joaquin; Vancanneyt, Guy; Perez, Ana G.; Sanz, Carlos; Stoermann, Katja; Rosahl, Sabine; Sanchez-Serrano, Jose J.
CS Cent. Nac. Biotecnol., CSIC, Madrid, 28049, Spain
SO Journal of Biological Chemistry (1996), 271(35), 21012-21019 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Lipoxygenases are ubiquitous enzymes in eukaryotes. In plants, lipoxygenases are involved in the synthesis of the hormone jasmonic acid that regulates plant responses to wounding and, in addn., is an inducer of tuberization in potato. We have isolated potato lipoxygenase cDNA clones. From their deduced amino acid sequences, three distinct classes are defined (Lox1, Lox2, and Lox3). They are encoded in gene families that display organ-specific expression, lox1 being expressed mostly in tubers and roots, lox2 in leaves, and lox3 in leaves and roots. Consistent with their organ-specific expression pattern, Lox1 expressed in bacteria preferentially uses as substrate linoleic acid, abundant in membrane lipids of tubers, whereas linolenic acid, prevalent in leaves, is the preferred substrate for the other two classes of lipoxygenases. Analyses on reaction products of the enzymes expressed in bacteria reveal that Lox1 primarily produces 9-hydroperoxides. In contrast, the jasmonic acid precursor, 13-hydroperoxylinolenic acid, is the major product of the action of Lox2 and Lox3 on linolenic acid. Upon wounding, the levels of Lox2 and Lox3 transcripts rise markedly in leaves. While Lox3 mRNA accumulation peaks as early as 30 min after wounding, Lox2 shows a steady increase over a 24-h time course, suggesting different roles for these lipoxygenase isoforms in the synthesis of the plant hormone jasmonic acid.
OSC.G 128 THERE ARE 128 CAPLUS RECORDS THAT CITE THIS RECORD (130 CITINGS)

L12 ANSWER 276 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:504328 CAPLUS <<LOGINID::20100206>>
DN 125:158858
OREF 125:29495a,29498a
TI Identification and Characterization of an Estrogen-Responsive Element Binding Protein Repressed by Estradiol
AU Gray, Wesley G.; Gorski, Jack
CS Department of Biochemistry, University of Wisconsin Madison, Madison, WI, 53706-1569, USA
SO Biochemistry (1996), 35(36), 11685-11692 CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
AB Cytosolic proteins from uteri of 19-day-old rats were analyzed by an electrophoresis mobility shift assay (EMSA) using a 31 base pair DNA probe contg. an estrogen-responsive element (ERE) from the vitellogenin A2 gene. EMSA identified three distinct cytosolic protein-DNA complexes that are separable by Q-Sepharose anion exchange chromatog. into an estrogen receptor (ER)-contg. fraction (150 mM NaCl eluate) and a non-ER-contg. fraction (250 mM NaCl eluate). We thus refer to the non-ER fraction as the ERE binding protein (ERE-BP). The ERE-BP-contg. fraction was repressed to 40-50% of its normal levels following a single injection of estradiol. In addn., ERE-BP levels were repressed to the same extent (greater than 50%) by day 20 of the rat's gestational period. Examn. of the ***expression*** ***pattern*** of ERE-BP shows that this ***activity*** is ***differentially*** expressed in both estrogen-responsive and nonresponsive tissues, with the highest levels of expression occurring in the pituitary. We next examd. the specificity of ERE-BP binding by competition anal. using DNA sequences corresponding to binding sites of several known transcription factors. ERE-BP was found to be specific for both the ER binding site (ERE) and TATA binding protein binding sites. Furthermore, satn. anal. demonstrated that ERE-BP binds to the ERE and TATA binding protein sequences with an apparent Kd of 1.2 and 0.12 nM, resp. Partial purifn. of ERE-BP using three chromatog. steps (Q-Sepharose, hydroxyapatite, and Sephacryl S300) followed by SDS anal. indicated the presence of three major protein bands (p102, p81, and p48) as judged by Coomassie staining. UV crosslinking of the ERE-BP/DNA complex followed by SDS-PAGE anal. indicates that the 48 kDa band seen in the final, partially purified fraction correlates with the ERE-BP activity. Thus, this study has identified a unique uterine cytosolic protein that binds to the ER binding site and may influence ER binding.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L12 ANSWER 277 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:437095 CAPLUS <<LOGINID::20100206>>
DN 125:106901
OREF 125:19835a
TI Direct analysis of the transcription of Escherichia coli rnpB gene harbored in a multicopy plasmid during bacterial growth
AU Park, Jeong Won; Jung, Young Hwan; Park, Bo Hyun; Jeoung, Yeon-Hee; Lee, Younghoon
CS Dep. Chem., Korea Advanced Inst. Sci. Technol., Taejon, 305-701, S. Korea
SO Journal of Biochemistry and Molecular Biology (1996), 29(3), 221-224 CODEN: JBMBE5; ISSN: 1225-8687
PB Biochemical Society of the Republic of Korea
DT Journal
LA English
AB To examine the growth-phase dependent control of Escherichia coli rnpB gene we used a combination of Northern anal. for RNA detn. and Southern anal. for plasmid DNA detn. The relative amts. of metabolically unstable transcript derived from the internally deleted rnpB gene harbored on a multicopy plasmid as well as the relative plasmid contents were measured by Northern anal. and Southern anal., resp., of total nucleic acids from E. coli cells contg. the plasmid. The relative transcription activity of the rnpB was represented by a ratio of the relative amt. of the transcript to that of the plasmid DNA during bacterial growth. The rnpB transcription increased rapidly with time during exponential growth, but started to decrease before the

transition period of an exponential growing cell culture into the stationary phase. Although the ***expression*** ***pattern*** was similar to the ***changes*** of .beta.-galactosidase ***activity*** expressed from the lysogenic strain carrying the chromosomal rnpB-lacZ fusion which were shown in a previous work, the present data appears to represent a more actual growth-phase control of the rnpB transcription than the previous data by the .beta.-galactosidase assay. In addn. the present method described for a direct anal. of both RNA and plasmid DNA provides a rapid and efficient method that can applied to an examn. of transcription control by using a multicopy plasmid.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L12 ANSWER 278 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:348583 CAPLUS <<LOGINID::20100206>>
DN 125:55968
OREF 125:10769a,10772a
TI Expression pattern of activation and adhesion molecules on peripheral blood CD4+ T-lymphocytes in relapsing-remitting multiple sclerosis patients: a serial analysis
AU Stueber, A.; Martin, R.; Stone, L. A.; Maloni, H.; McFarland, H. F.
CS Neuroimmunology Branch, National Institute of Neurological Disorders and Stroke, National Institutes of Health, Building 10, Room 5B-16, 10 Center DR MSC 1400, Bethesda, MD, 20892-1400, USA
SO Journal of Neuroimmunology (1996), 66(1-2), 147-151
CODEN: JNRIDW; ISSN: 0165-5728
PB Elsevier
DT Journal
LA English
AB We studied the expression of various cell surface mols. (CD25, CD28, CD29, CD45RO, CD56, LFA-1, VLA-4) on peripheral blood CD4+ T-cells in 6 relapsing-remitting multiple sclerosis (RR-MS) patients. Furthermore, ***changes*** in the ***expression*** ***pattern*** of these surface markers during intervals of increased disease ***activity*** , which was measured by gadolinium (Gd-DTPA) magnetic resonance imaging (MRI) were examd. Although several patients showed signs of increased disease activity during the observation period, this was not paralleled by a relevant change in the expression of these activation and adhesion mols.

L12 ANSWER 279 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:249240 CAPLUS <<LOGINID::20100206>>
DN 124:306223
OREF 124:56415a,56418a
TI Metabotropic glutamate receptors: potential drug targets
AU Knoepfel, Thomas; Gasparini, Fabrizio
CS CNS Research, Basel, CH-4002, Switz.
SO Drug Discovery Today (1996), 1(3), 103-8 CODEN: DDTOFS; ISSN: 1359-6446
PB Elsevier
DT Journal; General Review
LA English
AB A review, with 74 refs. The neurotransmitter glutamate activates not only ionotropic receptors, which mediate fast excitatory synaptic transmission, but also metabotropic receptors. The latter form a large, heterogeneous family of G protein-coupled receptors with specific functions in normal as well as in pathol. situations. The diverse cellular responses mediated by metabotropic glutamate receptors and their distinct ***expression*** ***patterns*** in ***different*** brain systems render these receptors potential ***drug*** targets with a variety of possible mechanisms of action.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L12 ANSWER 280 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:129375 CAPLUS <<LOGINID::20100206>>
DN 124:195024
OREF 124:35855a,35858a
TI Molecular neurobiology and pharmacology of the vasopressin/oxytocin receptor family
AU Peter, J.; Burbach, H.; Adan, Roger A. H.; Lolait, Stephen J.; van Leeuwen, Fred W.; Mezey, Eva; Palkovits, Miklos; Barberis, Claude
CS Rudolf Magnus Institute Neurosciences, Utrecht University, Utrecht, 3584 CG, Neth.
SO Cellular and Molecular Neurobiology (1995), 15(5), 573-95
CODEN: CMNEDI; ISSN: 0272-4340
PB Plenum
DT Journal; General Review
LA English
AB A review with 96 refs. summarizing recent insights in the pharmacol. properties, structure ***activity*** relationships, species ***differences*** in ligand specificity, ***expression*** ***patterns*** , and signal transduction of VP/OT receptor. The existence of addnl. VP/OT receptor subtypes is also discussed.
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

L12 ANSWER 281 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:77754 CAPLUS <<LOGINID::20100206>>
DN 124:136943
OREF 124:25247a,25250a
TI Analysis of differential gene expression by display of 3' end restriction fragments of cDNAs
AU Prashar, Yatindra; Weissman, Sherman M.
CS Dep. Genetics, Yale Univ. School of Medicine, New Haven, CT, 06510, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1996), 93(2), 659-63 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The authors have developed an approach to study changes in gene expression by selective PCR amplification and display of 3' end restriction fragments of double-stranded cDNAs. This method produces highly consistent and reproducible patterns, can detect almost all mRNAs in a sample, and can resolve hidden differences such as bands that differ in their sequence but comigrate on a gel. Bands corresponding to known cDNAs move to predictable positions on the gel, making this a powerful approach to correlate gel patterns with cDNA data bases. Applying this method, we have examd. ***differences*** in gene ***expression*** ***patterns*** during T-cell ***activation*** . Of a total of 700 bands that were evaluated in this study, as many as 3-4% represented mRNAs that are upregulated, while .apprxeq.2% were down-regulated within 4 h of activation of Jurkat T cells. These and other results suggest that this approach is suitable for the systematic, expeditious, and nearly exhaustive elucidation of subtle changes in the patterns of gene expression in cells with altered physiol. states.

OSC.G 111 THERE ARE 111 CAPLUS RECORDS THAT CITE THIS RECORD (111 CITINGS)

L12 ANSWER 282 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:23597 CAPLUS <<LOGINID::20100206>>
DN 124:82366
OREF 124:15349a,15352a
TI A study of different (CaMV 35S and mas) promoter activities and risk assessment of field use in transgenic rapeseed plants.
AU Pauk, J.; Stefanov, I.; Fekete, S.; Bogre, L.; Karsai, I.; Feher, A.; Dudits, D.
CS Cereal Research Institute, Szeged, H-6701, Hung.
SO Euphytica (1995), 85(1-3), 411-16 CODEN: EUPHAA; ISSN: 0014-2336
PB Kluwer
DT Journal
LA English
AB Gene fusions between the .beta.-glucuronidase (GUS) reporter gene and the promoters of the cauliflower mosaic virus 35S RNA transcript (CaMV 35S) and the mannopine synthase (mas) genes were introduced into rapeseed varieties via Agrobacterium-mediated transformation. Fluorometric assay of GUS ***activity*** indicated ***different*** ***expression*** ***patterns*** for the two promoters. In seedlings, the CaMV 35S promoter had max. activity in the primary roots, while the mas promoter was most active in the cotyledons. Etiolated seedlings cultured in the dark showed reduced activity of the mas promoter. Before vernalization at the rosette stage, both promoters were more active in older plant parts than in younger ones. At this stage, the highest activity was recorded in cotyledons. After the plants had bolted, reduced promoter function was detected in the upper parts of the transformed plants. Both promoters were functional in the majority of the studied organs of transgenic rapeseed plants, but the promoter activity varied between the organs at different developmental stages. The ability of pollen to transfer the introduced genes to other varieties and related species (e.g. Brassica napus and Diplotaxus muralis) by cross-pollination was studied in greenhouse expts., and field trials were carried out to est. the distance for biol.-relevant gene dispersal. In artificial crossing, the introduced marker gene was transferable into other varieties of Brassica napus. In field trials, at a distance of 1 m from the source of transgenic plants, the frequency of an outcrossing event was relatively high (10-3). Resistant individuals were found at 16 and 32 m from the transgenic pollen donors, but the frequency of an outcrossing event dropped to 10-5.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L12 ANSWER 283 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:888601 CAPLUS <<LOGINID::20100206>>
DN 124:25784
OREF 124:4875a,4878a
TI Specific and different expression patterns of two members of the leaf thionin multigene family of barley in transgenic tobacco
AU Holtorf, Soenke; Apel, Klaus; Bohlmann, Holger
CS Swiss Federal Institute of Technology (ETH), Institute of Plant Science, ETH-Zentrum, Universitaetstrasse 2, LFW D.58, Zurich, CH-8092, Switz
SO Plant Science (Shannon, Ireland) (1995), 111(1), 27-37
CODEN: PLSCE4; ISSN: 0168-9452
PB Elsevier
DT Journal
LA English
AB Thionins are cysteine-rich, basic, and toxic proteins that are assumed to be involved in the defense against pathogens. Barley (Hordeum vulgare L. cv.Carina) contains a large gene family coding for leaf-specific thionins that comprises more than 50 genes per haploid genome. How the expression of these variants is regulated was not known. To address this question, the authors have cloned 2 of these thionin genes, BTH6 and BTH7, each belonging to one of 2 subgroups, and analyzed their sequences. Both code for typical leaf thionin proteins. Their promoter regions have an identity of about 40% except for a region of 90 bp in the downstream region which has an identity of 80%. As reflected by these sequence differences, both promoters behave differently when placed in front of the uidA gene and analyzed in transgenic tobacco plants. Whereas the BTH6 promoter is constitutively expressed in most tissues of transgenic tobacco plants except the roots, the BTH7 promoter is only active in the vascular strands of the stem and older leaves. The BTH6 promoter is highly active in the epidermis and in xylem elements whereas the BTH7 promoter shows very high activity in phloem elements. In addn., both promoters are differently regulated by light. The BTH7 promoter is only active in the light. The BTH6 promoter shows a differential regulation in seedlings, being active in the hypocotyl in darkness but not in the cotyledons and vice versa in the light. These results indicate that the expression of the barley leaf thionin multigene family is regulated differentially at the transcriptional level.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L12 ANSWER 284 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:788567 CAPLUS <<LOGINID::20100206>>
DN 123:189299
OREF 123:33445a,33448a
TI Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
AU Lee, Norman H.; Weinstock, Keith G.; Kirkness, Ewen F.; Earle-Hughes, Julie A.; Fuldner, Rebecca A.; Marmaros, Simos; Glodek, Anna; Gocayne, Jeannine D.; Adams, Mark D.; et al.
CS Inst. Genomic Res., Gaithersburg, MD, 20878, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1995), 92(18), 8303-7 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB NGF-induced differentiation of adrenal chromaffin PC-12 cells to a neuronal phenotype involves alterations in gene expression and represents a model system to study neuronal differentiation. The authors have used the expressed-sequence-tag approach to identify .apprxeq.600 differentially expressed mRNAs in untreated and NGF-treated PC-12 cells that encode proteins with diverse structural and biochem. functions. Many of these mRNAs encode proteins belonging to cellular pathways not previously known to be regulated by NGF. Comparative expressed-sequence-tag anal. provides a basis for surveying global changes in gene-expression patterns in response to biol. signals at an unprecedented scale, is a powerful tool for identifying potential interactions between different cellular pathways, and allows the gene-expression profiles of individual genes belonging to a particular pathway to be followed.
OSC.G 161 THERE ARE 161 CAPLUS RECORDS THAT CITE THIS RECORD (161 CITINGS)

L12 ANSWER 285 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:778676 CAPLUS <<LOGINID::20100206>>
DN 123:281462
OREF 123:50335a,50338a
TI The expression pattern of the Distal-less homeobox-containing gene Dlx-5 in the developing chick limb bud suggests its involvement in apical ectodermal ridge activity, pattern formation, and cartilage differentiation
AU Ferrari, Deborah; Sumoy, Lauro; Gannon, Jennifer; Sun, Hailing; Brown, Anthony M. C.; Upholt, William B.; Kosher, Robert A.
CS Department of Anatomy, School of Medicine, University of Connecticut Health Center, Farmington, CT, 06030, USA
SO Mechanisms of Development (1995), 52(2,3), 257-64
CODEN: MEDVE6; ISSN: 0925-4773
PB Elsevier
DT Journal
LA English
AB The authors report the isolation from a chick limb bud cDNA library of a cDNA that contains the full coding sequence of chicken Dlx-5, a member of the Distal-less (Dlx) family of homeobox-contg. genes that encode homeodomains highly similar to that of the Drosophila Distal-less gene, a gene that is required for limb development in the Drosophila embryo. The expression pattern of Dlx-5 in the developing chick limb bud suggests that it may be involved in several aspects of limb morphogenesis. Dlx-5 is expressed in the apical ectodermal ridge (AER) which directs the outgrowth and patterning of underlying limb mesoderm. During early limb development Dlx-5 is also expressed in the mesoderm at the anterior margin of the limb bud and in a discrete group of mesodermal cells at the mid-proximal posterior margin that corresponds to the posterior necrotic zone. These mesodermal domains of Dlx-5 expression roughly correspond to the anterior and posterior boundaries of the progress zone, the group of highly proliferating undifferentiated mesodermal cells underneath the AER that will give rise to the skeletal elements of the limb and assocd. structures. The AER and anterior and posterior mesodermal domains of Dlx-5 expression are regions in which the homeobox-contg. gene Msx-2 is also highly expressed, suggesting that Dlx-5 and Msx-2 might be involved in regulatory networks that control AER activity and demarcate the progress zone. In addn., Dlx-5 is expressed in high amts. by the differentiating cartilaginous skeletal elements of the limb, suggesting it may be involved in regulating the onset of limb cartilage differentiation.
OSC.G 64 THERE ARE 64 CAPLUS RECORDS THAT CITE THIS RECORD (64 CITINGS)

L12 ANSWER 286 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:642538 CAPLUS <<LOGINID::20100206>>
DN 123:281451
OREF 123:50331a,50334a
TI Zebrafish wnt8 and wnt8b share a common activity but are involved in distinct developmental pathways
AU Kelly, Gregory M.; Greenstein, Penny; Erezyilmaz, Deniz F.; Moon, Randall T.
CS Sch. Med., Univ. Washington, Seattle, WA, 98195, USA
SO Development (Cambridge, United Kingdom) (1995), 121(6), 1787-99 CODEN: DEVPED; ISSN: 0950-1991
PB Company of Biologists
DT Journal
LA English
AB The specification of the vertebrate body plan is dependent on numerous signaling mols., including members of the Wnt family. The authors have identified two zebrafish wnt8 paralogs related to Xwnt-8B and Xwnt-8, resp. A RT-PCR assay demonstrated that wnt8 is expressed maternally, with transcripts detected throughout embryogenesis, whereas wnt8b transcripts were first detected during late gastrulation. The wnt8 transcripts at 50% epiboly are spatially restricted to those cells at the blastoderm margin, overlying gsc-expressing cells in the axial hypoblast. During late gastrulation, wnt8 was no longer detected in the marginal cells at the dorsal midline and by mid-segmentation, transcripts were found in the presumptive tail bud. In contrast, wnt8b expression is spatially restricted to prospective neuroepithelium, and later to neural-specific structures. Overexpression of both wants results in two major phenotypes: radialized embryos and embryos with anterior defects. These phenotypes were preceded by significant ***changes*** in the spatial ***expression*** ***patterns*** of gsc and ntl transcripts, reminiscent of ***activities*** of Xwnt-8 in Xenopus, and consistent with a role for wnt8 in the specification or patterning of mesoderm.
OSC.G 133 THERE ARE 133 CAPLUS RECORDS THAT CITE THIS RECORD (133 CITINGS)

L12 ANSWER 287 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:514332 CAPLUS <<LOGINID::20100206>>
DN 123:5662
OREF 123:1171a,1174a
TI Temporal and spatial expression patterns of PHYA and PHYB genes in Arabidopsis
AU Somers, David E.; Quail, Peter H.
CS Department of Plant Biology, University of California, Berkeley, CA, 94720, USA
SO Plant Journal (1995), 7(3), 413-27 CODEN: PLJUED; ISSN: 0960-7412
DT Journal
LA English
AB Phytochromes A and B have discrete photosensory functions in Arabidopsis. To det. whether differential temporal or spatial expression patterns of the PHYA and PHYB genes contribute to this phenomenon the expression of PHYA-GUS and PHYB-GUS reporter genes has been examd. in transgenic Arabidopsis. Histochem. and quant. biochem. analyses indicate that both transgenes are expressed extensively throughout the plant, including roots, shoots and flowers, during the entire life cycle, but with strong differences between the two in expression level and photoregulation, and more limited differences in spatial expression patterns. The data indicate that regulation is at the transcriptional level. In dry seeds, PHYB-GUS is expressed throughout the embryo at 3-fold higher levels than PHYA-GUS, which is confined primarily to the embryonic root tip. By contrast, PHYA promoter activity, despite strong neg. regulation in shoots by light, is consistently higher than PHYB (2-20-fold) in both the light and dark in most tissues during all subsequent developmental phases, from seedling to mature adult. At the tissue level, most cells appear to express both transgenes at some level at all stages examd., with highest apparent activity in vascular tissue and root tips. With the notable exception of pollen, where high PHYB-GUS but not PHYA-GUS expression occurs, few major differences are obsd. in the quant. spatial distribution pattern between the two transgenes. The strongly similar spatial and temporal ***expression*** ***patterns*** of PHYA-GUS and PHYB-GUS transgenes suggest that the ***differential*** photosensory ***activity*** of these two phytochromes occurs largely through differences in their (1) intrinsic biochem. activities, (2) relative abundances, and/or (3) independent and sep. reaction

partners, rather than through discrete, developmentally controlled expression patterns.
OSC.G 60 THERE ARE 60 CAPLUS RECORDS THAT CITE THIS RECORD (60 CITINGS)

L12 ANSWER 288 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:291275 CAPLUS <<LOGINID::20100206>>
DN 122:102818
OREF 122:19303a,19306a
TI Quantitative analysis of folylpolyglutamate synthetase gene expression in tumor tissues by the polymerase chain reaction: Marked variation of expression among leukemia patients
AU Lenz, Heinz-Josef; Danenberg, Kathleen; Schnieders, Barbara; Goeker, Erdem; Peters, Godefridus J.; Garrow, Tim; Shane, Barry; Bertino, Joseph R.; Danenberg, Peter V.
CS Kenneth T. Norris Jr. Cancer Hospital, University Southern California, Los Angeles, CA, 90033, USA
SO Oncology Research (1994), 6(7), 329-35 CODEN: ONREE8; ISSN: 0965-0407
PB Elsevier
DT Journal
LA English
AB Evidence from previous in vitro studies indicates that the enzyme folylpolyglutamate synthetase (FPGS) may be an important determinant of the antitumor activity of antifolate drugs that are substrates for this enzyme. To facilitate investigations regarding the assocn. between FPGS content of tumor tissues and the sensitivity of tumors to antifolates, we developed a polymerase chain reaction (PCR)-based gene expression quantitation assay for measuring relative amts. of FPGS mRNA in tumor tissue specimens. From the known sequence of the human gene, FPGS-specific PCR primers were chosen that flanked a 263-base segment of the FPGS gene. The PCR carried out with these primers was linear over at least a three orders of magnitude range of starting cDNA concn. The amt. of cDNA required per assay corresponded to the quantity of RNA contained in nanogram to microgram amts. of tissue, depending on the level of gene expression. In CHO AUXB1 (FPGS) cell lines transfected with human DNA and expressing ***different*** levels of human FPGS, FPGS gene ***expression*** ***measured*** by this assay was linear with the FPGS enzyme ***activity*** in the cells. In human head and neck cell lines, which contained naturally varying levels of FPGS enzyme activity, FPGS gene expressions were also linearly proportional to FPGS enzyme content as measured both by activity in cell-free exts. and by intracellular methotrexate polyglutamate formation. Among leukemic cells from 11 acute lymphocytic leukemia and acute myelogenous leukemia patients, FPGS expression varied by over 500-fold. This broad range of FPGS expression in tumors from different patients coupled with the availability of a sensitive and accurate assay for gene expression should now make it possible to establish whether FPGS expression in tumors is predictive for response to therapy involving short-term exposures to antifolates.
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)

L12 ANSWER 289 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:240309 CAPLUS <<LOGINID::20100206>>
DN 120:240309
OREF 120:42449a,42452a
TI Differential activity of the mannopine synthase and the CaMV 35S promoters during development of transgenic rapeseed plants
AU Stefanov, Ivan; Fekete, Sandor; Bogre, Laszlo; Pauk, Janos; Feher, Attila; Dudits, Denes
CS Inst. Plant Biol., Hung. Acad. Sci., Szeged, H-6701, Hung.
SO Plant Science (Shannon, Ireland) (1994), 95(2), 175-86 CODEN: PLSCE4; ISSN: 0168-9452
DT Journal
LA English
AB Fusions of the promoter of the cauliflower mosaic virus 35S RNA transcript (CaMV 35S) and the mannopine synthase (mas) gene to the .beta.-glucuronidase (GUS) reporter gene have been introduced into various cultivars of Brassica napus via Agrobacterium-mediated transformation. Transgenic rapeseed plants have been also regenerated from winter cultivars (Santana, Arabella) by shoot induction from kanamycin-resistant callus tissues on the medium supplemented with $AgNO_3$. Transformations was confirmed by Southern hybridization of genomic DNA from primary transformants and PCR anal. of DNA from second generation seedlings. .beta.-Glucuronidase ***activity*** analyzed by fluorometric assay or histochem. staining indicated a ***differential*** ***expression*** ***pattern*** for the two promoters. Organogenesis from in vitro cultured callus tissues was coupled with a relative increase of CaMV 35S promoter activity and redn. of mas promoter function. In seedlings, the CaMV 35S promoter had max. activity in the primary roots, while the mas promoter was the most active in the cotyledons. Etiolated seedlings, cultured in dark, showed reduced activity of the mas promoter. At rosette stage, both promoters were more active in elder plant parts than in younger ones. The highest activity values were recorded in cotyledons. After bolting, reduced promoter function was detected in upper parts of the transformed plants. Histol. staining showed that the CaMV 35S promoter was active in the cortex, the phloem and the vascular cambium, while the mas promoter directed gene expression in the phloem. In conclusion, both promoters were found to be functional in majority of the studied organs of transgenic rapeseed plants, however the promoter activity varied considerably between organs and tissues at various developmental stages.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L12 ANSWER 290 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:98211 CAPLUS <<LOGINID::20100206>>
DN 120:98211
OREF 120:17275a,17278a
TI cDNA analyses in the human genome project
AU Matsubara, Kenichi; Okubo, Kousaku
CS Inst. Mol. Cell. Biol., Osaka Univ., Suita, 565, Japan
SO Gene (1993), 135(1-2), 265-74 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB The ultimate goal of the human genome project is to decode all the genetic information carried in the genome. Towards this goal, the phys. structure of the genome, as well as the functional aspects of the genome, must be understood. The authors initiated a cDNA project to collect the 'expression profiles' of all human genes, a database with which to describe which genes are expressed, and to what extent, in any given human cell at a particular time. Single-cycle sequencing of randomly selected members from a 3'-directed cDNA library is most appropriate for this purpose: the sequence data serve as a 'gene signature' to identify the expression gene, and the frequency of appearance of the gene signature reflects the activity of the gene. The compiled data, which usually cover some 1000 sequencing results

per sample, are referred to as an 'expression profile.'. The authors applied this anal. to HepG2 (a cell line derived from a hepatocellular carcinoma), liver cells and lung cells. The expression profiles shed some light upon the unique features of gene expression in the cell or tissue tested. A comparison of the ***expression*** ***profiles*** among ***different*** cells has allowed ***active*** genes to be classified as housekeepers or those with cell-specific functions. A significant fraction of the abundantly expressed genes include those that are unique to the cell. In addn., the resulting collection of thousands of gene signatures is a useful source of probes for mapping and for isolating full-size cDNAs.
OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)

L12 ANSWER 291 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:50668 CAPLUS <<LOGINID::20100206>>
DN 120:50668
OREF 120:9219a
TI Tyrosine kinase receptors in the control of epithelial growth and morphogenesis during development
AU Birchmeier, Carmen; Sonnenberg, Eva; Weidner, K. Michael; Walter, Barbara
CS Max-Delbruck-Lab., Max-Planck-Ges., Cologne, 5000/30, Germany
SO BioEssays (1993), 15(3), 185-90 CODEN: BIOEEJ; ISSN: 0265-9247
DT Journal; General Review
LA English
AB A review, with 62 refs. The c-ros, c-met and c-neu genes encode receptor-type tyrosine kinases and were originally identified because of their oncogenic potential. However, recent progress in the anal. of these receptors and their resp. ligands indicate that they do not mediate exclusively mitogenic signals. Rather, they can induce cell movement, differentiation or morphogenesis of epithelial cells in culture. Interestingly, the discussed receptors are expressed in embryonal epithelia, whereas direct and indirect evidence shows that the corresponding ligands are produced in mesenchymal cells. In development, signals given by mesenchymal cells are major driving forces for differentiation and morphogenesis of epithelia; embryonal epithelia are generally unable to differentiate without the appropriate mesenchymal factors. The obsd. ***activities*** of these receptor/ligand systems in cultured cells and their ***expression*** ***patterns*** indicate that they regulate epithelial ***differentiation*** and morphogenesis also during embryogenesis and suggest thus a mol. basis for mesenchymal-epithelial interactions.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

L12 ANSWER 292 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1993:405230 CAPLUS <<LOGINID::20100206>>
DN 119:5230
OREF 119:1091a,1094a
TI A novel homeobox gene expressed in the anterior neural plate of the Xenopus embryo
AU Zaraiskii, A. G.; Lukyanov, S. A.; Vasil'evy, O. L.; Smirnov, Y. V.; Belyavskii, A. V.; Kazanskaya, O. V.
CS Shemyakin Inst. Chem., Moscow, 117871, Russia
SO Developmental Biology (Orlando, FL, United States) (1992), 152(2), 373-82 CODEN: DEBIAO; ISSN: 0012-1606
DT Journal
LA English
AB To obtain gene sequences controlling the early steps of amphibian neurogenesis, the authors have performed differential screening of a subtractive cDNA library prepd. by a novel PCR-based method from a single presumptive neural plate of a Xenopus laevis late-gastrula embryo. As a result the authors have isolated a fragment of a novel homeobox gene (named XANF-1, for Xenopus anterior neural folds). This gene is expressed predominantly in the anterior part of the developing nervous system. Such preferential localization of XANF-1 mRNA is established from its initially homogeneous distribution in ectoderm of early gastrula. This change in the ***expression*** ***pattern*** is conditioned by a ***differential*** influence of various mesoderm regions on ectoderm: anterior mesoderm ***activates*** XANF-1 expression in the overlying ectoderm, whereas posterior axial and ventral mesoderm areas inhibit it. Thus, selection of genes for specific expression in the central nervous system of the early vertebrate embryo is affected not only by chordamesoderm (a neural inductor) but also by ventral mesoderm.

L12 ANSWER 293 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1993:230539 CAPLUS <<LOGINID::20100206>>
DN 118:230539
OREF 118:39815a,39818a
TI ***Expression*** ***pattern*** of the ***activin*** receptor type IIA gene during ***differentiation*** of chick neural tissues, muscle and skin
AU Ohuchi, Hideyo; Noji, Sumihare; Koyama, Eiki; Myokai, Fumio; Nishikawa, Kiyoshi; Nohno, Tsutomu; Tashiro, Kosuke; Shiokawa, Koichiro; Matsuo, Nobuhiko; Taniguchi, Shigehiko
CS Med. Sch., Okayama Univ., Okayama, 700, Japan
SO FEBS Letters (1992), 303(2-3), 185-9 CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
AB To elucidate target cells of activins during embryogenesis, the authors isolated cDNAs of chick activin receptor type II (cActR-II) and studied expression patterns of the cActR-II gene by in situ hybridization. Transcripts of cActR-II were obsd. in neuroectoderm developing to spinal cord, brain and eyes, in surface ectoderm differentiating to epidermis, and in myotomes differentiating to muscles. The expression patterns of cActR-II suggest that activin and its receptor are involved in differentiation of chick neural tissues, muscle and skin after inducing the dorsal mesoderm.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

L12 ANSWER 294 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:569248 CAPLUS <<LOGINID::20100206>>
DN 117:169248
OREF 117:29235a,29238a
TI Cytokine gene expression in murine epidermal cell suspensions: interleukin 1 .beta. and macrophage inflammatory protein 1.alpha. are selectively expressed in Langerhans cells but are differentially regulated in culture
AU Heufler, Christine; Topar, Gerda; Koch, Franz; Trockenbacher, Bettina; Kaempgen, Eckhart; Romani, Nikolaus; Schuler, Gerold
CS Dep. Dermatol., Univ. Innsbruck, Innsbruck, A-6020, Austria
SO Journal of Experimental Medicine (1992), 176(4), 1221-6 CODEN: JEMEAV; ISSN: 0022-1007
DT Journal
LA English

AB Epidermal Langerhans cells (LC) are considered direct yet immature precursors of dendritic cells (DC) in the draining lymph nodes. Although the development of LC into potent immunostimulatory DC occurs in vitro and has been studied in detail, little is known about their profile of cytokine gene expression. By using reverse transcriptase polymerase chain reaction anal. to screen 16 cytokines followed by Northern blotting for selected anal., the cytokine gene ***expression*** ***profile*** of murine LC was detd. at ***different*** time points in culture when T cell stimulatory ***activity*** is increasing profoundly. LC regularly expressed macrophage inflammatory proteins, MIP-1.alpha. and MIP-2, and interleukin 1.beta. (IL-1.beta.). Both MIPs were downregulated upon culture and maturation into DC, whereas IL-1.beta. was strongly upregulated in culture. MIP-1.alpha. and IL-1.beta. mRNA were found only in LC, but not in other epidermal cells. Apart from trace amts. of IL-6 in cultured LC, several macrophage and T cell products were not detected. The cytokine expression profile of LC thus appears distinct from typical macrophages.
CSC.G 71 THERE ARE 71 CAPLUS RECORDS THAT CITE THIS RECORD (72 CITINGS)

L12 ANSWER 295 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:446277 CAPLUS<<LOGINID::20100206>>
DN 117:46277
OREF 117:8222h,8223a
TI Complement regulatory proteins at the feto-maternal interface during human placental development: distribution of CD59 by comparison with membrane cofactor protein (CD46) and decay accelerating factor (CD55)
AU Holmes, Christopher H.; Simpson, Karen L.; Okada, Hidechika; Okada, Noriko; Wainwright, Shane D.; Purcell, Damian F. J.; Houlihan, James M.
CS Dep. Obstet. Gynaecol., Univ. Bristol, Bristol, BS2 8EG, UK
SO European Journal of Immunology (1992), 22(6), 1579-85
CODEN: EJIMAF; ISSN: 0014-2980
DT Journal
LA English
AB The complement (C) regulatory proteins decay-accelerating factor (DAF, CD55) and membrane cofactor protein (MCP, CD46), which control C3 convertase, together with CD59, an inhibitor of the membrane attack complex (MAC), were found to be present in the developing human placenta from at least 6 wk of gestation until term. Immunostaining revealed differences in the distribution of these proteins on the fetally derived trophoblast epithelium, esp. in early placentae which contain trophoblast populations of diverse proliferative potential and differentiation status. Expression of all 3 proteins occurred on the terminally differentiated syncytiotrophoblast epithelium covering chorionic villi and which is in direct contact with material blood. CD59 was also expressed on the underlying villous cytotrophoblast cells and on their extravillous derivs. These 2 populations showed differential expression of the C3 convertase regulators. Villous cytotrophoblast cells expressed MCP but were largely devoid of DAF. Proliferation of this population to generate extravillous cytotrophoblast cell columns was assocd. with both an increase in DAF expression and a decrease in MCP expression. Throughout placental development, expression of DAF appeared to be lower than that of MCP and CD59 as assessed by solid-phase binding assays on isolated trophoblast membranes. Early placentae were also found to contain both DAF+ and DAF- chorionic villi. Conversely, expression of CD59 appeared comparatively high and transcripts for CD59 were much more abundant than those for DAF in purified trophoblast cells. C regulatory proteins appear to play an important role throughout gestation in protecting the fetally derived human conceptus from maternal C. The differential ***expression*** ***patterns*** of the proteins on trophoblast may reflect ***differences*** in requirement for specific functional ***activities*** at different locations within the placenta.
CSC.G 38 THERE ARE 38 CAPLUS RECORDS THAT CITE THIS RECORD (38 CITINGS)

L12 ANSWER 296 OF 296 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1990:549005 CAPLUS<<LOGINID::20100206>>
DN 113:149005
OREF 113:25248h,25249a
TI Indole-3-acetic acid content and glutamine synthetase activity in the pericarp, and peroxidase activity and isoenzymes in the meso- and exocarp of growing peach fruits
AU Sanchez-Roldan, Cristina; Heredia, Antonio; Valpuesta, Victoriano; Bukovac, Martin J.
CS Dep. Bioquim. Biol. Mol., Univ. Malaga, Malaga, 29071, Spain
SO Journal of Plant Growth Regulation (1990), 9(3), 171-4
CODEN: JPGRDI; ISSN: 0721-7595
DT Journal
LA English
AB IAA content in peach pericarp (Prunus persica) was highest at early stage I of development (.apprx.200 ng/g fresh wt.), decreased to the lowest level during stage II, and rose again at stage III to 60-70 ng/g fresh wt. High activity of glutamine synthetase was found in the pericarp during stage I. The sol. peroxidase activity was highest in the meso- and exocarp at stage II, and isoenzymic changes in this fraction corresponded to the transition from cationic isoenzymes, predominant at stage I, to anionic isoenzymes at stage III. The ionically bound peroxidase activity in these tissues was highest at stage I. The three developmental stages showed marked differences in auxin content and enzyme ***activities*** ; for peroxidases these ***changes*** reflect a developmental ***expression*** ***pattern*** for the isoenzymes.

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L2 5475133 S (DRUG? OR ACTIV?)/BI,AB
L3 47366 S L1 AND L2
L4 1652650 S L2 AND (CHANG? OR SHIFT? OR DIFFER?)/BI,AB
L5 1153 S (((EXPRESS?(W)PROFIL?) OR (EXPRESS?(W)PATTERN?) OR PROTEOM? O
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L12 296 S L11 NOT 2004/PY

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